



SEQUENCE LISTING

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<120> DIAGNOSIS AND TREATMENT OF MULTIPLE SULFATASE DEFICIENCY AND
OTHER SULFATASE DEFICIENCIES

<130> 10278-048001

<140> US 10/7⁷5,678

<141> 2004-02-10

<150> US 60/447,747

<151> 2003-02-11

<160> 96

<170> PatentIn version 3.2

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<212> DNA

<213> Homo sapiens

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Leu Cys Gly Ala Ala Gly Ser Gln Glu Ala Gly Thr Gly Ala Gly Ala
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Gly Ser Leu Ala Gly Ser Cys Gly Cys Gly Thr Pro Gln Arg Pro Gly
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gcc cat ggc agt tcg gca gcc gct cac cga tac tcg cgg gag gct aac 244
Ala His Gly Ser Ser Ala Ala Ala His Arg Tyr Ser Arg Glu Ala Asn
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| Val | Pro | Ile | Pro | Ala | Gly | Val | Phe | Thr | Met | Gly | Thr | Asp | Asp | Pro | Gln | |
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| Ile | Lys | Gln | Asp | Gly | Glu | Ala | Pro | Ala | Arg | Arg | Val | Thr | Ile | Asp | Ala | |
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| ttt | tac | atg | gat | gcc | tat | gaa | gtc | agt | aat | act | gaa | ttt | gag | aag | ttt | 436 |
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| gtg | aac | tca | act | ggc | tat | ttg | aca | gag | gct | gag | aag | ttt | ggc | gac | tcc | 484 |
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| Phe | Val | Phe | Glu | Gly | Met | Leu | Ser | Glu | Gln | Val | Lys | Thr | Asn | Ile | Gln | |
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| Trp | Ala | Gly | Lys | Arg | Leu | Pro | Thr | Glu | Ala | Glu | Trp | Glu | Tyr | Ser | Cys | |
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| cga | gga | ggc | ctg | cat | aat | aga | ctt | ttc | ccc | tgg | ggc | aac | aaa | ctg | cag | 772 |
| Arg | Gly | Gly | Leu | His | Asn | Arg | Leu | Phe | Pro | Trp | Gly | Asn | Lys | Leu | Gln | |
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| Pro | Lys | Gly | Gln | His | Tyr | Ala | Asn | Ile | Trp | Gln | Gly | Glu | Phe | Pro | Val | |
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| Thr | Asn | Thr | Gly | Glu | Asp | Gly | Phe | Gln | Gly | Thr | Ala | Pro | Val | Asp | Ala | |
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| ttc | cct | ccc | aat | ggt | tat | ggc | tta | tac | aac | ata | gtg | ggg | aac | gca | tgg | 916 |
| Phe | Pro | Pro | Asn | Gly | Tyr | Gly | Leu | Tyr | Asn | Ile | Val | Gly | Asn | Ala | Trp | |
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 Pro Gly Glu Arg Gln Leu Ala His Ser Lys Met Val Pro Ile Pro Ala
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 Gly Val Phe Thr Met Gly Thr Asp Asp Pro Gln Ile Lys Gln Asp Gly
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| Asn Arg Leu Phe Pro Trp Gly Asn Lys Leu Gln Pro Lys Gly Gln His | | | | |
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| Tyr Ala Asn Ile Trp Gln Gly Glu Phe Pro Val Thr Asn Thr Gly Glu | | | | |
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| Asp Gly Phe Gln Gly Thr Ala Pro Val Asp Ala Phe Pro Pro Asn Gly | | | | |
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| Tyr Gly Leu Tyr Asn Ile Val Gly Asn Ala Trp Glu Trp Thr Ser Asp | | | | |
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| Trp Trp Thr Val His His Ser Val Glu Glu Thr Leu Asn Pro Lys Gly | | | | |
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| Pro Pro Ser Gly Lys Asp Arg Val Lys Lys Gly Gly Ser Tyr Met Cys | | | | |
| | | 325 | | 330 |
| | | | | 335 |
| His Arg Ser Tyr Cys Tyr Arg Tyr Arg Cys Ala Ala Arg Ser Gln Asn | | | | |
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| tgcagctgct | ccctgggtgg | tacctgtgaa | aggcgctaac | tggagacacc | cagaagggcc | 600 |
| tgactctact | attctgcaca | ggccggatca | tccagttctc | catgtgtcct | ggaatgatgc | 660 |
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| ccagcattat | gccaacattt | ggcagggcga | ttttccggtg | accaacactg | gtgaggatgg | 840 |
| cttccaagga | actgcgcctg | ttgatgcctt | ccctcccaat | ggttatggct | tataacaacat | 900 |
| agtggggaac | gcatgggaat | ggacttcaga | ctggtggact | gttcatcatt | ctgttgaaga | 960 |
| aacgcttaac | ccaaaaggtc | ccccttctgg | gaaagaccga | gtgaagaaag | gtggatccta | 1020 |
| catgtgccat | aggtcttatt | gttacaggta | tcgctgtgct | gctcggagcc | agaacacacc | 1080 |
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Ala Ala Ala His Arg Tyr Ser Arg Glu Ala Asn Ala Pro Gly Pro Val
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Gly Val Phe Thr Met Gly Thr Asp Asp Pro Gln Ile Lys Gln Asp Gly
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Tyr Leu Thr Glu Ala Glu Lys Phe Gly Asp Ser Phe Val Phe Glu Gly
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 180 185 190

Gly Pro Asp Ser Thr Ile Leu His Arg Pro Asp His Pro Val Leu His
 195 200 205

Val Ser Trp Asn Asp Ala Val Ala Tyr Cys Thr Trp Ala Gly Lys Arg
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Leu Pro Thr Glu Ala Glu Trp Glu Tyr Ser Cys Arg Gly Gly Leu His
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Tyr Ala Asn Ile Trp Gln Gly Asp Phe Pro Val Thr Asn Thr Gly Glu
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Asp Gly Phe Gln Gly Thr Ala Pro Val Asp Ala Phe Pro Pro Asn Gly
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Thr Thr Asp Ala Leu Asn Val Leu Leu Ile Ile Val Asp Asp Leu Arg
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Pro Ser Leu Gly Cys Tyr Gly Asp Lys Leu Val Arg Ser Pro Asn Ile

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| | | | | |
|---|-----|-----|-----|-----|
| 50 | | 55 | | 60 |
| Asp Gln Leu Ala Ser His Ser Leu Leu Phe Gln Asn Ala Phe Ala Gln | | | | |
| 65 | | 70 | | 75 |
| | | | | 80 |
| Gln Ala Val Cys Ala Pro Ser Arg Val Ser Phe Leu Thr Gly Arg Arg | | | | |
| | 85 | | 90 | 95 |
| Pro Asp Thr Thr Arg Leu Tyr Asp Phe Asn Ser Tyr Trp Arg Val His | | | | |
| | 100 | | 105 | 110 |
| Ala Gly Asn Phe Ser Thr Ile Pro Gln Tyr Phe Lys Glu Asn Gly Tyr | | | | |
| | 115 | | 120 | 125 |
| Val Thr Met Ser Val Gly Lys Val Phe His Pro Gly Ile Ser Ser Asn | | | | |
| | 130 | | 135 | 140 |
| His Thr Asp Asp Ser Pro Tyr Ser Trp Ser Phe Pro Pro Tyr His Pro | | | | |
| 145 | | 150 | | 155 |
| | | | | 160 |
| Ser Ser Glu Lys Tyr Glu Asn Thr Lys Thr Cys Arg Gly Pro Asp Gly | | | | |
| | 165 | | 170 | 175 |
| Glu Leu His Ala Asn Leu Leu Cys Pro Val Asp Val Leu Asp Val Pro | | | | |
| | 180 | | 185 | 190 |
| Glu Gly Thr Leu Pro Asp Lys Gln Ser Thr Glu Gln Ala Ile Gln Leu | | | | |
| | 195 | | 200 | 205 |
| Leu Glu Lys Met Lys Thr Ser Ala Ser Pro Phe Phe Leu Ala Val Gly | | | | |
| | 210 | | 215 | 220 |
| Tyr His Lys Pro His Ile Pro Phe Arg Tyr Pro Lys Glu Phe Gln Lys | | | | |
| 225 | | 230 | | 235 |
| | | | | 240 |
| Leu Tyr Pro Leu Glu Asn Ile Thr Leu Ala Pro Asp Pro Glu Val Pro | | | | |
| | 245 | | 250 | 255 |
| Asp Gly Leu Pro Pro Val Ala Tyr Asn Pro Trp Met Asp Ile Arg Gln | | | | |
| | 260 | | 265 | 270 |
| Arg Glu Asp Val Gln Ala Leu Asn Ile Ser Val Pro Tyr Gly Pro Ile | | | | |
| | 275 | | 280 | 285 |

Pro Val Asp Phe Gln Arg Lys Ile Arg Gln Ser Tyr Phe Ala Ser Val
 290 295 300

Ser Tyr Leu Asp Thr Gln Val Gly Arg Leu Leu Ser Ala Leu Asp Asp
 305 310 315 320

Leu Gln Leu Ala Asn Ser Thr Ile Ile Ala Phe Thr Ser Asp His Gly
 325 330 335

Trp Ala Leu Gly Glu His Gly Glu Trp Ala Lys Tyr Ser Asn Phe Asp
 340 345 350

Val Ala Thr His Val Pro Leu Ile Phe Tyr Val Pro Gly Arg Thr Ala
 355 360 365

Ser Leu Pro Glu Ala Gly Glu Lys Leu Phe Pro Tyr Leu Asp Pro Phe
 370 375 380

Asp Ser Ala Ser Gln Leu Met Glu Pro Gly Arg Gln Ser Met Asp Leu
 385 390 395 400

Val Glu Leu Val Ser Leu Phe Pro Thr Leu Ala Gly Leu Ala Gly Leu
 405 410 415

Gln Val Pro Pro Arg Cys Pro Val Pro Ser Phe His Val Glu Leu Cys
 420 425 430

Arg Glu Gly Lys Asn Leu Leu Lys His Phe Arg Phe Arg Asp Leu Glu
 435 440 445

Glu Asp Pro Tyr Leu Pro Gly Asn Pro Arg Glu Leu Ile Ala Tyr Ser
 450 455 460

Gln Tyr Pro Arg Pro Ser Asp Ile Pro Gln Trp Asn Ser Asp Lys Pro
 465 470 475 480

Ser Leu Lys Asp Ile Lys Ile Met Gly Tyr Ser Ile Arg Thr Ile Asp
 485 490 495

Tyr Arg Tyr Thr Val Trp Val Gly Phe Asn Pro Asp Glu Phe Leu Ala
 500 505 510

Asn Phe Ser Asp Ile His Ala Gly Glu Leu Tyr Phe Val Asp Ser Asp
 515 520 525

Pro Leu Gln Asp His Asn Met Tyr Asn Asp Ser Gln Gly Gly Asp Leu
 530 535 540

Phe Gln Leu Leu Met Pro
 545 550

<210> 8
 <211> 2657
 <212> DNA
 <213> Homo sapiens

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 ctctgccggg cgcgccccg gaacgcactg ctgtctctcg cggatgacgg aggctttgag 120
 agtggcgcggt acaacaacag cgccatcgcc acccgcacc tggacgcctt ggcccgccgc 180
 agcctcctct ttcgcaatgc cttcacctcg gtcagcagct gctctcccag ccgcgccagc 240
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 cacttcaact ccttcgacaa ggtgcggagc ctgccgctgc tgctcagcca agctggtgtg 360
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 gcgtacacgg aggagaatgg ctccgtcctc cagggtggggc ggaacatcac tagaattaag 480
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 gccgctcagt acaccaccgt cggccgcatg gaccaaggag ttggactggt gctccaggag 780
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 ggctcgaaga ccatccacct cactggccgg tccctcctgc cggcgctgga ggccgagccc 1080
 ctctgggcca ccgtctttgg cagccagagc caccacgagg tcaccatgtc ctaccccatg 1140

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gtgggcagta cgcaggctcc accgacactc acctgggagc acggcgctg gctcttacca 2040
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caccctcgg cctggacacc cctcgaagga gagggcgctt ccttgagtag gtgggctccc 2580
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tattgtaaaa gcttttt 2657

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<210> 9
<211> 502
<212> PRT
<213> Homo sapiens

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<400> 9

Met Ser Cys Pro Val Pro Ala Cys Cys Ala Leu Leu Leu Val Leu Gly
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Leu Cys Arg Ala Arg Pro Arg Asn Ala Leu Leu Leu Leu Ala Asp Asp
 20 25 30

Gly Gly Phe Glu Ser Gly Ala Tyr Asn Asn Ser Ala Ile Ala Thr Pro
 35 40 45

His Leu Asp Ala Leu Ala Arg Arg Ser Leu Leu Phe Arg Asn Ala Phe
 50 55 60

Thr Ser Val Ser Ser Cys Ser Pro Ser Arg Ala Ser Leu Leu Thr Gly
 65 70 75 80

Leu Pro Gln His Gln Asn Gly Met Tyr Gly Leu His Gln Asp Val His
 85 90 95

His Phe Asn Ser Phe Asp Lys Val Arg Ser Leu Pro Leu Leu Leu Ser
 100 105 110

Gln Ala Gly Val Arg Thr Gly Ile Ile Gly Lys Lys His Val Gly Pro
 115 120 125

Glu Thr Val Tyr Pro Phe Asp Phe Ala Tyr Thr Glu Glu Asn Gly Ser
 130 135 140

Val Leu Gln Val Gly Arg Asn Ile Thr Arg Ile Lys Leu Leu Val Arg
 145 150 155 160

Lys Phe Leu Gln Thr Gln Asp Asp Arg Pro Phe Phe Leu Tyr Val Ala
 165 170 175

Phe His Asp Pro His Arg Cys Gly His Ser Gln Pro Gln Tyr Gly Thr
 180 185 190

Phe Cys Glu Lys Phe Gly Asn Gly Glu Ser Gly Met Gly Arg Ile Pro
 195 200 205

Asp Trp Thr Pro Gln Ala Tyr Asp Pro Leu Asp Val Leu Val Pro Tyr
 210 215 220

Phe Val Pro Asn Thr Pro Ala Ala Arg Ala Asp Leu Ala Ala Gln Tyr
 225 230 235 240

Thr Thr Val Gly Arg Met Asp Gln Gly Val Gly Leu Val Leu Gln Glu
 245 250 255

Leu Arg Asp Ala Gly Val Leu Asn Asp Thr Leu Val Ile Phe Thr Ser
 260 265 270

Asp Asn Gly Ile Pro Phe Pro Ser Gly Arg Thr Asn Leu Tyr Trp Pro
 275 280 285

Gly Thr Ala Glu Pro Leu Leu Val Ser Ser Pro Glu His Pro Lys Arg
 290 295 300

Trp Gly Gln Val Ser Glu Ala Tyr Val Ser Leu Leu Asp Leu Thr Pro
 305 310 315 320

Thr Ile Leu Asp Trp Phe Ser Ile Pro Tyr Pro Ser Tyr Ala Ile Phe
 325 330 335

Gly Ser Lys Thr Ile His Leu Thr Gly Arg Ser Leu Leu Pro Ala Leu
 340 345 350

Glu Ala Glu Pro Leu Trp Ala Thr Val Phe Gly Ser Gln Ser His His
 355 360 365

Glu Val Thr Met Ser Tyr Pro Met Arg Ser Val Gln His Arg His Phe
 370 375 380

Arg Leu Val His Asn Leu Asn Phe Lys Met Pro Phe Pro Ile Asp Gln
 385 390 395 400

Asp Phe Tyr Val Ser Pro Thr Phe Gln Asp Leu Leu Asn Arg Thr Thr
 405 410 415

Ala Gly Gln Pro Thr Gly Trp Tyr Lys Asp Leu Arg His Tyr Tyr Tyr
 420 425 430

Arg Ala Arg Trp Glu Leu Tyr Asp Arg Ser Arg Asp Pro His Glu Thr
 435 440 445

Gln Asn Leu Ala Thr Asp Pro Arg Phe Ala Gln Leu Leu Glu Met Leu
 450 455 460

Arg Asp Gln Leu Ala Lys Trp Gln Trp Glu Thr His Asp Pro Trp Val
 465 470 475 480

Cys Ala Pro Asp Gly Val Leu Glu Glu Lys Leu Ser Pro Gln Cys Gln
 485 490 495

Pro Leu His Asn Glu Leu
 500

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 <211> 1014
 <212> DNA
 <213> Homo sapiens

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 gagtgagact gtctcagaac agcaacaaca aaatgcccgc tgctgctggg tccagaagag 180
 cttgaataac tgcattgttct ttttctcaat tttcatttcc cagaactggg cacctccggg 240
 ctgtgaaaag ttagggaagt gtctgacacc tccagaatcc attcccaaga agtgcctctg 300
 gtcccactag cacctgcgca gactcaggcc aggcctagaa tctccagttg gccctgcaag 360
 tgccctggagg aaggatggct ctggcctcgg tcctccccca accctgcca agccagacag 420
 acagcacctg cagacgcagg gggactgcac aattccacct gccaggacc tgaccctggc 480
 gtgtgcttgg cctcctcctc cgcccacggc gcctcagatt tcaggaccct cctcctcgcc 540
 cacggcgcct cagacctcag gaccctgccg tctcacgcct ttgtgaaccc caaatatctg 600
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 cctgacaaca ggtgcccag gtggctgggg atacagtttg cttttataca tcttagggag 720
 acacaagatc agtatgtgta tggcgtacat tggttcagtc agccttccac tgaatacacg 780
 attgagtctg gccagtgaa tccgcatttt tatgtaaaca gtaagggaac ggggcaatca 840
 tataagcggt tgtctcagg gagccccaga gggatgactt ccagttccgt ctgtcctttg 900
 tccacaagga atttccctgg gcgctaatta tgaggaggc gtgtagcttc ttatcattgt 960
 agctatgtta tttagaaata aaacgggagg caggtttgcc taattcccag gttg 1014

<210> 11
 <211> 522
 <212> PRT
 <213> Homo sapiens

<400> 11

Met Ala Ala Val Val Ala Ala Thr Arg Trp Trp Gln Leu Leu Leu Val
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Leu Ser Ala Ala Gly Met Gly Ala Ser Gly Ala Pro Gln Pro Pro Asn
 20 25 30

Ile Leu Leu Leu Leu Met Asp Asp Met Gly Trp Gly Asp Leu Gly Val
 35 40 45

Tyr Gly Glu Pro Ser Arg Glu Thr Pro Asn Leu Asp Arg Met Ala Ala
 50 55 60

Glu Gly Leu Leu Phe Pro Asn Phe Tyr Ser Ala Asn Pro Leu Cys Ser
 65 70 75 80

Pro Ser Arg Ala Ala Leu Leu Thr Gly Arg Leu Pro Ile Arg Asn Gly
 85 90 95

Phe Tyr Thr Thr Asn Ala His Ala Arg Asn Ala Tyr Thr Pro Gln Glu
 100 105 110

Ile Val Gly Gly Ile Pro Asp Ser Glu Gln Leu Leu Pro Glu Leu Leu
 115 120 125

Lys Lys Ala Gly Tyr Val Ser Lys Ile Val Gly Lys Trp His Leu Gly
 130 135 140

His Arg Pro Gln Phe His Pro Leu Lys His Gly Phe Asp Glu Trp Phe
 145 150 155 160

Gly Ser Pro Asn Cys His Phe Gly Pro Tyr Asp Asn Lys Ala Arg Pro
 165 170 175

Asn Ile Pro Val Tyr Arg Asp Trp Glu Met Val Gly Arg Tyr Tyr Glu
 180 185 190

Glu Phe Pro Ile Asn Leu Lys Thr Gly Glu Ala Asn Leu Thr Gln Ile

| 195 | 200 | 205 |
|--|-----|-----|
| Tyr Leu Gln Glu Ala Leu Asp Phe Ile Lys Arg Gln Ala Arg His His 210 215 220 | | |
| Pro Phe Phe Leu Tyr Trp Ala Val Asp Ala Thr His Ala Pro Val Tyr 225 230 235 240 | | |
| Ala Ser Lys Pro Phe Leu Gly Thr Ser Gln Arg Gly Arg Tyr Gly Asp 245 250 255 | | |
| Ala Val Arg Glu Ile Asp Asp Ser Ile Gly Lys Ile Leu Glu Leu Leu 260 265 270 | | |
| Gln Asp Leu His Val Ala Asp Asn Thr Phe Val Phe Phe Thr Ser Asp 275 280 285 | | |
| Asn Gly Ala Ala Leu Ile Ser Ala Pro Glu Gln Gly Gly Ser Asn Gly 290 295 300 | | |
| Pro Phe Leu Cys Gly Lys Gln Thr Thr Phe Glu Gly Gly Met Arg Glu 305 310 315 320 | | |
| Pro Ala Leu Ala Trp Trp Pro Gly His Val Thr Ala Gly Gln Val Ser 325 330 335 | | |
| His Gln Leu Gly Ser Ile Met Asp Leu Phe Thr Thr Ser Leu Ala Leu 340 345 350 | | |
| Ala Gly Leu Thr Pro Pro Ser Asp Arg Ala Ile Asp Gly Leu Asn Leu 355 360 365 | | |
| Leu Pro Thr Leu Leu Gln Gly Arg Leu Met Asp Arg Pro Ile Phe Tyr 370 375 380 | | |
| Tyr Arg Gly Asp Thr Leu Met Ala Ala Thr Leu Gly Gln His Lys Ala 385 390 395 400 | | |
| His Phe Trp Thr Trp Thr Asn Ser Trp Glu Asn Phe Arg Gln Gly Ile 405 410 415 | | |
| Asp Phe Cys Pro Gly Gln Asn Val Ser Gly Val Thr Thr His Asn Leu 420 425 430 | | |

Glu Asp His Thr Lys Leu Pro Leu Ile Phe His Leu Gly Arg Asp Pro
 435 440 445

Gly Glu Arg Phe Pro Leu Ser Phe Ala Ser Ala Glu Tyr Gln Glu Ala
 450 455 460

Leu Ser Arg Ile Thr Ser Val Val Gln Gln His Gln Glu Ala Leu Val
 465 470 475 480

Pro Ala Gln Pro Gln Leu Asn Val Cys Asn Trp Ala Val Met Asn Trp
 485 490 495

Ala Pro Pro Gly Cys Glu Lys Leu Gly Lys Cys Leu Thr Pro Pro Glu
 500 505 510

Ser Ile Pro Lys Lys Cys Leu Trp Ser His
 515 520

<210> 12
 <211> 2379
 <212> DNA
 <213> Homo sapiens

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 cggcgggggca gcccccgcca cctgccctcc tgcagcccag cgctgctact gctgggtgctg 180
 ggcgggtgcc tgggggtctt cgggggtggct gcgggaaccc ggaggcccaa cgtgggtgctg 240
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 gctctcatcg gagagatggg gatgactttt tccagtgttt atgtgccaag tgctctctgc 360
 tgccccagca gagccagtat cctgacagga aagtaccac ataatcatca cgttgtgaac 420
 aacactctgg aggggaactg cagtagtaag tcctggcaga agatccaaga accaaatact 480
 ttcccagcaa ttctcagatc aatgtgtggt tatcagacct tttttgcagg gaaatattta 540
 aatgagtacg gagccccaga tgcaggtgga ctagaacacg ttctcttggg ttggagttac 600
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 gcacggaagc atggtgaaaa ctatagtgtg gactacctga cagatgtttt ggctaattgtc 720
 tccttgagct ttctggacta caagtccaac tttgagcct tcttcattgat gatcgccact 780

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| ccagcgctc attcgcttg gacagctgca cctcagtacc agaaggcttt ccagaatgtc | 840 |
| tttgcaccaa gaaacaagaa cttcaacatc catggaacga acaagcactg gttaattagg | 900 |
| caagccaaga ctccaatgac taattcttca atacagtttt tagataatgc atttaggaaa | 960 |
| aggtggcaaa ctctcctctc agttgatgac cttgtggaga aactgggtcaa gaggctggag | 1020 |
| ttcactgggg agctcaacaa cacttacatc ttctatacct cagacaatgg ctatcacaca | 1080 |
| ggacagtttt ccttgccaat agacaagaga cagctgtatg agtttgatat caaagttcca | 1140 |
| ctgttggttc gaggacctgg gatcaaacca aatcagacaa gcaagatgct ggttgccaac | 1200 |
| attgacttgg gtctactat tttggacatt gctggctacg acctaaataa gacacagatg | 1260 |
| gatgggatgt ccttattgcc cattttgaga ggtgccagta acttgacctg gcgatcagat | 1320 |
| gtcctgggtg aataccaagg agaaggccgt aacgtcactg acccaacatg cccttccttg | 1380 |
| agtctggcg tatctcaatg cttcccagac tgtgtatgtg aagatgctta taacaatacc | 1440 |
| tatgcctgtg tgaggacaat gtcagcattg tggaatttgc agtattgcga gtttgatgac | 1500 |
| caggaggtgt ttgtagaagt ctataatctg actgcagacc cagaccagat cactaacatt | 1560 |
| gctaaaacca tagaccaga gcttttagga aagatgaact atcggttaat gatgttacag | 1620 |
| tcctgttctg ggccaacctg tcgcactcca ggggtttttg accccggata caggtttgac | 1680 |
| ccccgtctca tgttcagcaa tcgcggcagt gtcaggactc gaagattttc caaacatctt | 1740 |
| ctgtagcgac ctcacacagc ctctgcagat ggatccctgc acgcctcttt ctgatgaagt | 1800 |
| gattgtagta ggtgtctgta gctagtcttc aagaccacac ctggaagagt ttctgggctg | 1860 |
| gctttaagtc ctgtttgaaa aagcaacca gtcagctgac ttctctgtgc aatgtgttaa | 1920 |
| actgtgaact ctgcccattg gtcaggagtg gctgtctctg gtctcttctt ttagctgaca | 1980 |
| aggacactcc tgaggctctt gttctcactg ttttttttt atcctggggc cacagttctt | 2040 |
| gattattcct cttgtggtta aagactgaat ttgtaaaccc attcagataa atggcagtac | 2100 |
| tttaggacac acacaaacac acagatacac cttttgatat gtaagcttga cctaaagtca | 2160 |
| aaggacctgt gtagcatttc agattgagca cttcactatc aaaaatacta acatcacatg | 2220 |
| gcttgaagag taaccatcag agctgaatca tccaagtaag aacaagtacc attgttgatt | 2280 |
| gataagtaga gatacatctt ttatgatgtt catcacagtg tggttaagggt gcaaattcaa | 2340 |
| aacatgtcac ccaagctctg ttcattgttt tgtgaattc | 2379 |

<211> 552
 <212> PRT
 <213> Homo sapiens

<400> 13

Met Arg Leu Leu Pro Leu Ala Pro Gly Arg Leu Arg Arg Gly Ser Pro
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Arg His Leu Pro Ser Cys Ser Pro Ala Leu Leu Leu Leu Val Leu Gly
 20 25 30

Gly Cys Leu Gly Val Phe Gly Val Ala Ala Gly Thr Arg Arg Pro Asn
 35 40 45

Val Val Leu Leu Leu Thr Asp Asp Gln Asp Glu Val Leu Gly Gly Met
 50 55 60

Thr Pro Leu Lys Lys Thr Lys Ala Leu Ile Gly Glu Met Gly Met Thr
 65 70 75 80

Phe Ser Ser Ala Tyr Val Pro Ser Ala Leu Cys Cys Pro Ser Arg Ala
 85 90 95

Ser Ile Leu Thr Gly Lys Tyr Pro His Asn His His Val Val Asn Asn
 100 105 110

Thr Leu Glu Gly Asn Cys Ser Ser Lys Ser Trp Gln Lys Ile Gln Glu
 115 120 125

Pro Asn Thr Phe Pro Ala Ile Leu Arg Ser Met Cys Gly Tyr Gln Thr
 130 135 140

Phe Phe Ala Gly Lys Tyr Leu Asn Glu Tyr Gly Ala Pro Asp Ala Gly
 145 150 155 160

Gly Leu Glu His Val Pro Leu Gly Trp Ser Tyr Trp Tyr Ala Leu Glu
 165 170 175

Lys Asn Ser Lys Tyr Tyr Asn Tyr Thr Leu Ser Ile Asn Gly Lys Ala
 180 185 190

Arg Lys His Gly Glu Asn Tyr Ser Val Asp Tyr Leu Thr Asp Val Leu
 195 200 205

Ala Asn Val Ser Leu Asp Phe Leu Asp Tyr Lys Ser Asn Phe Glu Pro
 210 215 220

Phe Phe Met Met Ile Ala Thr Pro Ala Pro His Ser Pro Trp Thr Ala
 225 230 235 240

Ala Pro Gln Tyr Gln Lys Ala Phe Gln Asn Val Phe Ala Pro Arg Asn
 245 250 255

Lys Asn Phe Asn Ile His Gly Thr Asn Lys His Trp Leu Ile Arg Gln
 260 265 270

Ala Lys Thr Pro Met Thr Asn Ser Ser Ile Gln Phe Leu Asp Asn Ala
 275 280 285

Phe Arg Lys Arg Trp Gln Thr Leu Leu Ser Val Asp Asp Leu Val Glu
 290 295 300

Lys Leu Val Lys Arg Leu Glu Phe Thr Gly Glu Leu Asn Asn Thr Tyr
 305 310 315 320

Ile Phe Tyr Thr Ser Asp Asn Gly Tyr His Thr Gly Gln Phe Ser Leu
 325 330 335

Pro Ile Asp Lys Arg Gln Leu Tyr Glu Phe Asp Ile Lys Val Pro Leu
 340 345 350

Leu Val Arg Gly Pro Gly Ile Lys Pro Asn Gln Thr Ser Lys Met Leu
 355 360 365

Val Ala Asn Ile Asp Leu Gly Pro Thr Ile Leu Asp Ile Ala Gly Tyr
 370 375 380

Asp Leu Asn Lys Thr Gln Met Asp Gly Met Ser Leu Leu Pro Ile Leu
 385 390 395 400

Arg Gly Ala Ser Asn Leu Thr Trp Arg Ser Asp Val Leu Val Glu Tyr
 405 410 415

Gln Gly Glu Gly Arg Asn Val Thr Asp Pro Thr Cys Pro Ser Leu Ser
 420 425 430

Pro Gly Val Ser Gln Cys Phe Pro Asp Cys Val Cys Glu Asp Ala Tyr
 435 440 445

Asn Asn Thr Tyr Ala Cys Val Arg Thr Met Ser Ala Leu Trp Asn Leu
 450 455 460

Gln Tyr Cys Glu Phe Asp Asp Gln Glu Val Phe Val Glu Val Tyr Asn
 465 470 475 480

Leu Thr Ala Asp Pro Asp Gln Ile Thr Asn Ile Ala Lys Thr Ile Asp
 485 490 495

Pro Glu Leu Leu Gly Lys Met Asn Tyr Arg Leu Met Met Leu Gln Ser
 500 505 510

Cys Ser Gly Pro Thr Cys Arg Thr Pro Gly Val Phe Asp Pro Gly Tyr
 515 520 525

Arg Phe Asp Pro Arg Leu Met Phe Ser Asn Arg Gly Ser Val Arg Thr
 530 535 540

Arg Arg Phe Ser Lys His Leu Leu
 545 550

<210> 14
 <211> 2022
 <212> DNA
 <213> Homo sapiens

<400> 14
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 tctccgctcg agaatctgaa ggtgccctgg tcttgaggga gttccgtccc agccctgcgg 180
 tctcccggta ctgctcgccc cggccctctg gagcttcagg aggcggccgt cagggtcggg 240
 gagtatttgg gtccggggtc tcagggaagg gcggcgctg ggtctgcggt atcggaaga 300
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 cccagctct accactccca acctggacca gctggcgggc ggagggctgc ggttcacaga 540
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<210> 15
<211> 507
<212> PRT
<213> Homo sapiens

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<400> 15

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Val Ala Arg Pro Pro Asn Ile Val Leu Ile Phe Ala Asp Asp Leu Gly
20 25 30

Tyr Gly Asp Leu Gly Cys Tyr Gly His Pro Ser Ser Thr Thr Pro Asn
35 40 45

Leu Asp Gln Leu Ala Ala Gly Gly Leu Arg Phe Thr Asp Phe Tyr Val
50 55 60

Pro Val Ser Leu Cys Thr Pro Ser Arg Ala Ala Leu Leu Thr Gly Arg
65 70 75 80

Leu Pro Val Arg Met Gly Met Tyr Pro Gly Val Leu Val Pro Ser Ser
85 90 95

Arg Gly Gly Leu Pro Leu Glu Glu Val Thr Val Ala Glu Val Leu Ala
100 105 110

Ala Arg Gly Tyr Leu Thr Gly Met Ala Gly Lys Trp His Leu Gly Val
115 120 125

Gly Pro Glu Gly Ala Phe Leu Pro Pro His Gln Gly Phe His Arg Phe
130 135 140

Leu Gly Ile Pro Tyr Ser His Asp Gln Gly Pro Cys Gln Asn Leu Thr
145 150 155 160

Cys Phe Pro Pro Ala Thr Pro Cys Asp Gly Gly Cys Asp Gln Gly Leu
165 170 175

Val Pro Ile Pro Leu Leu Ala Asn Leu Ser Val Glu Ala Gln Pro Pro
180 185 190

Trp Leu Pro Gly Leu Glu Ala Arg Tyr Met Ala Phe Ala His Asp Leu
195 200 205

Met Ala Asp Ala Gln Arg Gln Asp Arg Pro Phe Phe Leu Tyr Tyr Ala
210 215 220

Ser His His Thr His Tyr Pro Gln Phe Ser Gly Gln Ser Phe Ala Glu

| | | | | | | |
|---|--|-----|--|-----|--|-----|
| 225 | | 230 | | 235 | | 240 |
| Arg Ser Gly Arg Gly Pro Phe Gly Asp Ser Leu Met Glu Leu Asp Ala | | | | | | |
| | | 245 | | 250 | | 255 |
| Ala Val Gly Thr Leu Met Thr Ala Ile Gly Asp Leu Gly Leu Leu Glu | | | | | | |
| | | 260 | | 265 | | 270 |
| Glu Thr Leu Val Ile Phe Thr Ala Asp Asn Gly Pro Glu Thr Met Arg | | | | | | |
| | | 275 | | 280 | | 285 |
| Met Ser Arg Gly Gly Cys Ser Gly Leu Leu Arg Cys Gly Lys Gly Thr | | | | | | |
| | | 290 | | 295 | | 300 |
| Thr Tyr Glu Gly Gly Val Arg Glu Pro Ala Leu Ala Phe Trp Pro Gly | | | | | | |
| 305 | | 310 | | 315 | | 320 |
| His Ile Ala Pro Gly Val Thr His Glu Leu Ala Ser Ser Leu Asp Leu | | | | | | |
| | | 325 | | 330 | | 335 |
| Leu Pro Thr Leu Ala Ala Leu Ala Gly Ala Pro Leu Pro Asn Val Thr | | | | | | |
| | | 340 | | 345 | | 350 |
| Leu Asp Gly Phe Asp Leu Ser Pro Leu Leu Leu Gly Thr Gly Lys Ser | | | | | | |
| | | 355 | | 360 | | 365 |
| Pro Arg Gln Ser Leu Phe Phe Tyr Pro Ser Tyr Pro Asp Glu Val Arg | | | | | | |
| | | 370 | | 375 | | 380 |
| Gly Val Phe Ala Val Arg Thr Gly Lys Tyr Lys Ala His Phe Phe Thr | | | | | | |
| 385 | | 390 | | 395 | | 400 |
| Gln Gly Ser Ala His Ser Asp Thr Thr Ala Asp Pro Ala Cys His Ala | | | | | | |
| | | 405 | | 410 | | 415 |
| Ser Ser Ser Leu Thr Ala His Glu Pro Pro Leu Leu Tyr Asp Leu Ser | | | | | | |
| | | 420 | | 425 | | 430 |
| Lys Asp Pro Gly Glu Asn Tyr Asn Leu Leu Gly Gly Val Ala Gly Ala | | | | | | |
| | | 435 | | 440 | | 445 |
| Thr Pro Glu Val Leu Gln Ala Leu Lys Gln Leu Gln Leu Leu Lys Ala | | | | | | |
| | | 450 | | 455 | | 460 |

Gln Leu Asp Ala Ala Val Thr Phe Gly Pro Ser Gln Val Ala Arg Gly
 465 470 475 480

Glu Asp Pro Ala Leu Gln Ile Cys Cys His Pro Gly Cys Thr Pro Arg
 485 490 495

Pro Ala Cys Cys His Cys Pro Asp Pro His Ala
 500 505

<210> 16
 <211> 2228
 <212> DNA
 <213> Homo sapiens

<400> 16
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<210> 17
<211> 533
<212> PRT
<213> Homo sapiens

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<400> 17
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Met Gly Pro Arg Gly Ala Ala Ser Leu Pro Arg Gly Pro Gly Pro Arg
1           5           10           15

```

```

Arg Leu Leu Leu Pro Val Val Leu Pro Leu Leu Leu Leu Leu Leu
20           25           30

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Ala Pro Pro Gly Ser Gly Ala Gly Ala Ser Arg Pro Pro His Leu Val
35           40           45

```

Phe Leu Leu Ala Asp Asp Leu Gly Trp Asn Asp Val Gly Phe His Gly
50 55 60

Ser Arg Ile Arg Thr Pro His Leu Asp Ala Leu Ala Ala Gly Gly Val
65 70 75 80

Leu Leu Asp Asn Tyr Tyr Thr Gln Pro Leu Cys Thr Pro Ser Arg Ser
85 90 95

Gln Leu Leu Thr Gly Arg Tyr Gln Ile Arg Thr Gly Leu Gln His Gln
100 105 110

Ile Ile Trp Pro Cys Gln Pro Ser Cys Val Pro Leu Asp Glu Lys Leu
115 120 125

Leu Pro Gln Leu Leu Lys Glu Ala Gly Tyr Thr Thr His Met Val Gly
130 135 140

Lys Trp His Leu Gly Met Tyr Arg Lys Glu Cys Leu Pro Thr Arg Arg
145 150 155 160

Gly Phe Asp Thr Tyr Phe Gly Tyr Leu Leu Gly Ser Glu Asp Tyr Tyr
165 170 175

Ser His Glu Arg Cys Thr Leu Ile Asp Ala Leu Asn Val Thr Arg Cys
180 185 190

Ala Leu Asp Phe Arg Asp Gly Glu Glu Val Ala Thr Gly Tyr Lys Asn
195 200 205

Met Tyr Ser Thr Asn Ile Phe Thr Lys Arg Ala Ile Ala Leu Ile Thr
210 215 220

Asn His Pro Pro Glu Lys Pro Leu Phe Leu Tyr Leu Ala Leu Gln Ser
225 230 235 240

Val His Glu Pro Leu Gln Val Pro Glu Glu Tyr Leu Lys Pro Tyr Asp
245 250 255

Phe Ile Gln Asp Lys Asn Arg His His Tyr Ala Gly Met Val Ser Leu
260 265 270

Met Asp Glu Ala Val Gly Asn Val Thr Ala Ala Leu Lys Ser Ser Gly
 275 280 285

Leu Trp Asn Asn Thr Val Phe Ile Phe Ser Thr Asp Asn Gly Gly Gln
 290 295 300

Thr Leu Ala Gly Gly Asn Asn Trp Pro Leu Arg Gly Arg Lys Trp Ser
 305 310 315 320

Leu Trp Glu Gly Gly Val Arg Gly Val Gly Phe Val Ala Ser Pro Leu
 325 330 335

Leu Lys Gln Lys Gly Val Lys Asn Arg Glu Leu Ile His Ile Ser Asp
 340 345 350

Trp Leu Pro Thr Leu Val Lys Leu Ala Arg Gly His Thr Asn Gly Thr
 355 360 365

Lys Pro Leu Asp Gly Phe Asp Val Trp Lys Thr Ile Ser Glu Gly Ser
 370 375 380

Pro Ser Pro Arg Ile Glu Leu Leu His Asn Ile Asp Pro Asn Phe Val
 385 390 395 400

Asp Ser Ser Pro Cys Pro Arg Asn Ser Met Ala Pro Ala Lys Asp Asp
 405 410 415

Ser Ser Leu Pro Glu Tyr Ser Ala Phe Asn Thr Ser Val His Ala Ala
 420 425 430

Ile Arg His Gly Asn Trp Lys Leu Leu Thr Gly Tyr Pro Gly Cys Gly
 435 440 445

Tyr Trp Phe Pro Pro Pro Ser Gln Tyr Asn Val Ser Glu Ile Pro Ser
 450 455 460

Ser Asp Pro Pro Thr Lys Thr Leu Trp Leu Phe Asp Ile Asp Arg Asp
 465 470 475 480

Pro Glu Glu Arg His Asp Leu Ser Arg Glu Tyr Pro His Ile Val Thr
 485 490 495

Lys Leu Leu Ser Arg Leu Gln Phe Tyr His Lys His Ser Val Pro Val
 500 505 510

Tyr Phe Pro Ala Gln Asp Pro Arg Cys Asp Pro Lys Ala Thr Gly Val
 515 520 525

Trp Gly Pro Trp Met
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<210> 18
 <211> 2401
 <212> DNA
 <213> Homo sapiens

<400> 18
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 accatgaaca gaggatgaac aagtgaagtt gcaatctcct ccatcacagc tcagttcccc 180
 aacaacagga tcacaagctg gagatgcctt taaggaagat gaagatccct ttctctctac 240
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<210> 19
<211> 583
<212> PRT
<213> Homo sapiens

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<400> 19
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Met Pro Leu Arg Lys Met Lys Ile Pro Phe Leu Leu Leu Phe Phe Leu
1           5           10           15

```

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Trp Glu Ala Glu Ser His Ala Ala Ser Arg Pro Asn Ile Ile Leu Val
          20           25           30

```

Met Ala Asp Asp Leu Gly Ile Gly Asp Pro Gly Cys Tyr Gly Asn Lys
 35 40 45

Thr Ile Arg Thr Pro Asn Ile Asp Arg Leu Ala Ser Gly Gly Val Lys
 50 55 60

Leu Thr Gln His Leu Ala Ala Ser Pro Leu Cys Thr Pro Ser Arg Ala
 65 70 75 80

Ala Phe Met Thr Gly Arg Tyr Pro Val Arg Ser Gly Met Ala Ser Trp
 85 90 95

Ser Arg Thr Gly Val Phe Leu Phe Thr Ala Ser Ser Gly Gly Leu Pro
 100 105 110

Thr Asp Glu Ile Thr Phe Ala Lys Leu Leu Lys Asp Gln Gly Tyr Ser
 115 120 125

Thr Ala Leu Ile Gly Lys Trp His Leu Gly Met Ser Cys His Ser Lys
 130 135 140

Thr Asp Phe Cys His His Pro Leu His His Gly Phe Asn Tyr Phe Tyr
 145 150 155 160

Gly Ile Ser Leu Thr Asn Leu Arg Asp Cys Lys Pro Gly Glu Gly Ser
 165 170 175

Val Phe Thr Thr Gly Phe Lys Arg Leu Val Phe Leu Pro Leu Gln Ile
 180 185 190

Val Gly Val Thr Leu Leu Thr Leu Ala Ala Leu Asn Cys Leu Gly Leu
 195 200 205

Leu His Val Pro Leu Gly Val Phe Phe Ser Leu Leu Phe Leu Ala Ala
 210 215 220

Leu Ile Leu Thr Leu Phe Leu Gly Phe Leu His Tyr Phe Arg Pro Leu
 225 230 235 240

Asn Cys Phe Met Met Arg Asn Tyr Glu Ile Ile Gln Gln Pro Met Ser
 245 250 255

Tyr Asp Asn Leu Thr Gln Arg Leu Thr Val Glu Ala Ala Gln Phe Ile
 260 265 270

Gln Arg Asn Thr Glu Thr Pro Phe Leu Leu Val Leu Ser Tyr Leu His
 275 280 285

Val His Thr Ala Leu Phe Ser Ser Lys Asp Phe Ala Gly Lys Ser Gln
 290 295 300

His Gly Val Tyr Gly Asp Ala Val Glu Glu Met Asp Trp Ser Val Gly
 305 310 315 320

Gln Ile Leu Asn Leu Leu Asp Glu Leu Arg Leu Ala Asn Asp Thr Leu
 325 330 335

Ile Tyr Phe Thr Ser Asp Gln Gly Ala His Val Glu Glu Val Ser Ser
 340 345 350

Lys Gly Glu Ile His Gly Gly Ser Asn Gly Ile Tyr Lys Gly Gly Lys
 355 360 365

Ala Asn Asn Trp Glu Gly Gly Ile Arg Val Pro Gly Ile Leu Arg Trp
 370 375 380

Pro Arg Val Ile Gln Ala Gly Gln Lys Ile Asp Glu Pro Thr Ser Asn
 385 390 395 400

Met Asp Ile Phe Pro Thr Val Ala Lys Leu Ala Gly Ala Pro Leu Pro
 405 410 415

Glu Asp Arg Ile Ile Asp Gly Arg Asp Leu Met Pro Leu Leu Glu Gly
 420 425 430

Lys Ser Gln Arg Ser Asp His Glu Phe Leu Phe His Tyr Cys Asn Ala
 435 440 445

Tyr Leu Asn Ala Val Arg Trp His Pro Gln Asn Ser Thr Ser Ile Trp
 450 455 460

Lys Ala Phe Phe Phe Thr Pro Asn Phe Asn Pro Val Gly Ser Asn Gly
 465 470 475 480

Cys Phe Ala Thr His Val Cys Phe Cys Phe Gly Ser Tyr Val Thr His
485 490 495

His Asp Pro Pro Leu Leu Phe Asp Ile Ser Lys Asp Pro Arg Glu Arg
500 505 510

Asn Pro Leu Thr Pro Ala Ser Glu Pro Arg Phe Tyr Glu Ile Leu Lys
515 520 525

Val Met Gln Glu Ala Ala Asp Arg His Thr Gln Thr Leu Pro Glu Val
530 535 540

Pro Asp Gln Phe Ser Trp Asn Asn Phe Leu Trp Lys Pro Trp Leu Gln
545 550 555 560

Leu Cys Cys Pro Ser Thr Gly Leu Ser Cys Gln Cys Asp Arg Glu Lys
565 570 575

Gln Asp Lys Arg Leu Ser Arg
580

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<210> 20
<211> 1945
<212> DNA
<213> Homo sapiens
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| ggactctttg ccggtgctac tgtttttatg cttgcttctg aagacgtgtg aacctaaaac | 180 |
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| cttgcacgag catggctatg caaccggcct cataggaaaa tggcaccagg gtgtgaattg | 540 |
| tgcataccgc ggggatcact gccaccaccc cctgaaccac ggatttgact atttctacgg | 600 |
| catgcccttc acgctcacia acgactgtga ccagggcagg ccccccgaag tggacgccgc | 660 |
| cctgagggcg cagctctggg gttacacca gttcctggcg ctggggatto tcaccctggc | 720 |

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gagtctgtg cccagcagt tttccatgag caacatcctg tggaagccgt ggctgcagcc    1800
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gcttggttct atcttcagtc cggaa                                           1945

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<210> 21
<211> 593
<212> PRT
<213> Homo sapiens

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<400> 21
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Met Arg Ser Ala Ala Arg Arg Gly Arg Ala Ala Pro Ala Ala Arg Asp
1           5           10           15

```

```

Ser Leu Pro Val Leu Leu Phe Leu Cys Leu Leu Leu Lys Thr Cys Glu
20           25           30

```

Pro Lys Thr Ala Asn Ala Phe Lys Pro Asn Ile Leu Leu Ile Met Ala
 35 40 45

Asp Asp Leu Gly Thr Gly Asp Leu Gly Cys Tyr Gly Asn Asn Thr Leu
 50 55 60

Arg Thr Pro Asn Ile Asp Gln Leu Ala Glu Glu Gly Val Arg Leu Thr
 65 70 75 80

Gln His Leu Ala Ala Ala Pro Leu Cys Thr Pro Ser Arg Ala Ala Phe
 85 90 95

Leu Thr Gly Arg His Ser Phe Arg Ser Gly Met Asp Ala Ser Asn Gly
 100 105 110

Tyr Arg Ala Leu Gln Trp Asn Ala Gly Ser Gly Gly Leu Pro Glu Asn
 115 120 125

Glu Thr Thr Phe Ala Arg Ile Leu Gln Gln His Gly Tyr Ala Thr Gly
 130 135 140

Leu Ile Gly Lys Trp His Gln Gly Val Asn Cys Ala Ser Arg Gly Asp
 145 150 155 160

His Cys His His Pro Leu Asn His Gly Phe Asp Tyr Phe Tyr Gly Met
 165 170 175

Pro Phe Thr Leu Thr Asn Asp Cys Asp Pro Gly Arg Pro Pro Glu Val
 180 185 190

Asp Ala Ala Leu Arg Ala Gln Leu Trp Gly Tyr Thr Gln Phe Leu Ala
 195 200 205

Leu Gly Ile Leu Thr Leu Ala Ala Gly Gln Thr Cys Gly Phe Phe Ser
 210 215 220

Val Ser Ala Arg Ala Val Thr Gly Met Ala Gly Val Gly Cys Leu Phe
 225 230 235 240

Phe Ile Ser Trp Tyr Ser Ser Phe Gly Phe Val Arg Arg Trp Asn Cys
 245 250 255

Ile Leu Met Arg Asn His Asp Val Thr Glu Gln Pro Met Val Leu Glu
 260 265 270

Lys Thr Ala Ser Leu Met Leu Lys Glu Ala Val Ser Tyr Ile Glu Arg
 275 280 285

His Lys His Gly Pro Phe Leu Leu Phe Leu Ser Leu Leu His Val His
 290 295 300

Ile Pro Leu Val Thr Thr Ser Ala Phe Leu Gly Lys Ser Gln His Gly
 305 310 315 320

Leu Tyr Gly Asp Asn Val Glu Glu Met Asp Trp Leu Ile Gly Lys Val
 325 330 335

Leu Asn Ala Ile Glu Asp Asn Gly Leu Lys Asn Ser Thr Phe Thr Tyr
 340 345 350

Phe Thr Ser Asp His Gly Gly His Leu Glu Ala Arg Asp Gly His Ser
 355 360 365

Gln Leu Gly Gly Trp Asn Gly Ile Tyr Lys Gly Gly Lys Gly Met Gly
 370 375 380

Gly Trp Glu Gly Gly Ile Arg Val Pro Gly Ile Phe His Trp Pro Gly
 385 390 395 400

Val Leu Pro Ala Gly Arg Val Ile Gly Glu Pro Thr Ser Leu Met Asp
 405 410 415

Val Phe Pro Thr Val Val Gln Leu Val Gly Gly Glu Val Pro Gln Asp
 420 425 430

Arg Val Ile Asp Gly His Ser Leu Val Pro Leu Leu Gln Gly Ala Glu
 435 440 445

Ala Arg Ser Ala His Glu Phe Leu Phe His Tyr Cys Gly Gln His Leu
 450 455 460

His Ala Ala Arg Trp His Gln Lys Asp Ser Gly Ser Val Trp Lys Val
 465 470 475 480

His Tyr Thr Thr Pro Gln Phe His Pro Glu Glu Arg Gly Leu Leu Thr
485 490 495

Ala Glu Ala Ser Ala His Ala Glu Trp Gly Gly Val Thr His His Arg
500 505 510

Pro Pro Leu Leu Phe Asp Leu Ser Arg Asp Pro Ser Glu Ala Arg Pro
515 520 525

Leu Thr Pro Asp Ser Glu Pro Leu Tyr His Ala Val Ile Ala Arg Val
530 535 540

Gly Ala Ala Val Ser Glu His Arg Gln Thr Leu Ser Pro Val Pro Gln
545 550 555 560

Gln Phe Ser Met Ser Asn Ile Leu Trp Lys Pro Trp Leu Gln Pro Cys
565 570 575

Cys Gly His Phe Pro Phe Cys Ser Cys His Glu Asp Gly Asp Gly Thr
580 585 590

Pro

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<210> 22
<211> 1858
<212> DNA
<213> Homo sapiens
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| agacaacatg | ttacatctgc | accattcttg | tttgtgtttc | aggagctggc | tgccagcgat | | 120 |
| gctcgctgta | ctgctaagtt | tggcaccatc | agcttcacgc | gacatttccg | cctcccgacc | | 180 |
| gaacatcctt | cttctgatgg | cggacgacct | tggcattggg | gacattggct | gctatggcaa | | 240 |
| caacaccatg | aggactccga | atattgaccg | ccttgccagag | gacggcgtga | agctgaccca | | 300 |
| acacatctct | gccgcatctt | tgtgcacccc | aagcagagcc | gccttcctca | cgggcagata | | 360 |
| ccctgtgcga | tcagggatgg | tttccagcat | tggttaccgt | gttcttcagt | ggaccggagc | | 420 |
| atctggaggt | cttccaacaa | atgagacaac | ttttgcaaaa | atactgaaag | agaaaggcta | | 480 |
| tgccactgga | ctcattggaa | aatggcatct | gggtctcaac | tgtgagtcag | ccagtgatca | | 540 |
| ttgccaccac | cctctccatc | atggctttga | gcattttctac | ggaatgcctt | tctccttgat | | 600 |


```

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<210> 23
<211> 589
<212> PRT
<213> Homo sapiens

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<400> 23
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```

Met Leu His Leu His His Ser Cys Leu Cys Phe Arg Ser Trp Leu Pro
1           5           10          15

```

```

Ala Met Leu Ala Val Leu Leu Ser Leu Ala Pro Ser Ala Ser Ser Asp
20           25           30

```

Ile Ser Ala Ser Arg Pro Asn Ile Leu Leu Leu Met Ala Asp Asp Leu
 35 40 45

Gly Ile Gly Asp Ile Gly Cys Tyr Gly Asn Asn Thr Met Arg Thr Pro
 50 55 60

Asn Ile Asp Arg Leu Ala Glu Asp Gly Val Lys Leu Thr Gln His Ile
 65 70 75 80

Ser Ala Ala Ser Leu Cys Thr Pro Ser Arg Ala Ala Phe Leu Thr Gly
 85 90 95

Arg Tyr Pro Val Arg Ser Gly Met Val Ser Ser Ile Gly Tyr Arg Val
 100 105 110

Leu Gln Trp Thr Gly Ala Ser Gly Gly Leu Pro Thr Asn Glu Thr Thr
 115 120 125

Phe Ala Lys Ile Leu Lys Glu Lys Gly Tyr Ala Thr Gly Leu Ile Gly
 130 135 140

Lys Trp His Leu Gly Leu Asn Cys Glu Ser Ala Ser Asp His Cys His
 145 150 155 160

His Pro Leu His His Gly Phe Glu His Phe Tyr Gly Met Pro Phe Ser
 165 170 175

Leu Met Gly Asp Cys Ala Arg Trp Glu Leu Ser Glu Lys Arg Val Asn
 180 185 190

Leu Glu Gln Lys Leu Asn Phe Leu Phe Gln Val Leu Ala Leu Val Ala
 195 200 205

Leu Thr Leu Val Ala Gly Lys Leu Thr His Leu Ile Pro Val Ser Trp
 210 215 220

Met Pro Val Ile Trp Ser Ala Leu Ser Ala Val Leu Leu Leu Ala Ser
 225 230 235 240

Ser Tyr Phe Val Gly Ala Leu Ile Val His Ala Asp Cys Phe Leu Met
 245 250 255

Arg Asn His Thr Ile Thr Glu Gln Pro Met Cys Phe Gln Arg Thr Thr
 260 265 270

Pro Leu Ile Leu Gln Glu Val Ala Ser Phe Leu Lys Arg Asn Lys His
 275 280 285

Gly Pro Phe Leu Leu Phe Val Ser Phe Leu His Val His Ile Pro Leu
 290 295 300

Ile Thr Met Glu Asn Phe Leu Gly Lys Ser Leu His Gly Leu Tyr Gly
 305 310 315 320

Asp Asn Val Glu Glu Met Asp Trp Met Val Gly Arg Ile Leu Asp Thr
 325 330 335

Leu Asp Val Glu Gly Leu Ser Asn Ser Thr Leu Ile Tyr Phe Thr Ser
 340 345 350

Asp His Gly Gly Ser Leu Glu Asn Gln Leu Gly Asn Thr Gln Tyr Gly
 355 360 365

Gly Trp Asn Gly Ile Tyr Lys Gly Gly Lys Gly Met Gly Gly Trp Glu
 370 375 380

Gly Gly Ile Arg Val Pro Gly Ile Phe Arg Trp Pro Gly Val Leu Pro
 385 390 395 400

Ala Gly Arg Val Ile Gly Glu Pro Thr Ser Leu Met Asp Val Phe Pro
 405 410 415

Thr Val Val Arg Leu Ala Gly Gly Glu Val Pro Gln Asp Arg Val Ile
 420 425 430

Asp Gly Gln Asp Leu Leu Pro Leu Leu Leu Gly Thr Ala Gln His Ser
 435 440 445

Asp His Glu Phe Leu Met His Tyr Cys Glu Arg Phe Leu His Ala Ala
 450 455 460

Arg Trp His Gln Arg Asp Arg Gly Thr Met Trp Lys Val His Phe Val
 465 470 475 480

Thr Pro Val Phe Gln Pro Glu Gly Ala Gly Ala Cys Tyr Gly Arg Lys
 485 490 495

Val Cys Pro Cys Phe Gly Glu Lys Val Val His His Asp Pro Pro Leu
 500 505 510

Leu Phe Asp Leu Ser Arg Asp Pro Ser Glu Thr His Ile Leu Thr Pro
 515 520 525

Ala Ser Glu Pro Val Phe Tyr Gln Val Met Glu Arg Val Gln Gln Ala
 530 535 540

Val Trp Glu His Gln Arg Thr Leu Ser Pro Val Pro Leu Gln Leu Asp
 545 550 555 560

Arg Leu Gly Asn Ile Trp Arg Pro Trp Leu Gln Pro Cys Cys Gly Pro
 565 570 575

Phe Pro Leu Cys Trp Cys Leu Arg Glu Asp Asp Pro Gln
 580 585

<210> 24
 <211> 1996
 <212> DNA
 <213> Homo sapiens

<400> 24
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ccagaggaag cctttggtcc taacgagaag agataattac aatcaggcta ccaaaggaag 1920
cactaacttt ggtgctttca agttggcaag gagtgcattt aatagtcaat aaattcatct 1980
accattccag attatt 1996

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<210> 25
<211> 591
<212> PRT
<213> Homo sapiens

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<400> 25

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Met Arg Pro Arg Arg Pro Leu Val Phe Met Ser Leu Val Cys Ala Leu
1          5          10          15

```

Leu Asn Thr Trp Pro Gly His Thr Gly Cys Met Thr Thr Arg Pro Asn
 20 25 30

Ile Val Leu Ile Met Val Asp Asp Leu Gly Ile Gly Asp Leu Gly Cys
 35 40 45

Tyr Gly Asn Asp Thr Met Arg Thr Pro His Ile Asp Arg Leu Ala Arg
 50 55 60

Glu Gly Val Arg Leu Thr Gln His Ile Ser Ala Ala Ser Leu Cys Ser
 65 70 75 80

Pro Ser Arg Ser Ala Phe Leu Thr Gly Arg Tyr Pro Ile Arg Ser Gly
 85 90 95

Met Val Ser Ser Gly Asn Arg Arg Val Ile Gln Asn Leu Ala Val Pro
 100 105 110

Ala Gly Leu Pro Leu Asn Glu Thr Thr Leu Ala Ala Leu Leu Lys Lys
 115 120 125

Gln Gly Tyr Ser Thr Gly Leu Ile Gly Lys Trp His Gln Gly Leu Asn
 130 135 140

Cys Asp Ser Arg Ser Asp Gln Cys His His Pro Tyr Asn Tyr Gly Phe
 145 150 155 160

Asp Tyr Tyr Tyr Gly Met Pro Phe Thr Leu Val Asp Ser Cys Trp Pro
 165 170 175

Asp Pro Ser Arg Asn Thr Glu Leu Ala Phe Glu Ser Gln Leu Trp Leu
 180 185 190

Cys Val Gln Leu Val Ala Ile Ala Ile Leu Thr Leu Thr Phe Gly Lys
 195 200 205

Leu Ser Gly Trp Val Ser Val Pro Trp Leu Leu Ile Phe Ser Met Ile
 210 215 220

Leu Phe Ile Phe Leu Leu Gly Tyr Ala Trp Phe Ser Ser His Thr Ser
 225 230 235 240

Pro Leu Tyr Trp Asp Cys Leu Leu Met Arg Gly His Glu Ile Thr Glu

| | | | | | |
|---|-----|--|-----|--|-----|
| | 245 | | 250 | | 255 |
| Gln Pro Met Lys Ala Glu Arg Ala Gly Ser Ile Met Val Lys Glu Ala | 260 | | 265 | | 270 |
| Ile Ser Phe Leu Glu Arg His Ser Lys Glu Thr Phe Leu Leu Phe Phe | 275 | | 280 | | 285 |
| Ser Phe Leu His Val His Thr Pro Leu Pro Thr Thr Asp Asp Phe Thr | 290 | | 295 | | 300 |
| Gly Thr Ser Lys His Gly Leu Tyr Gly Asp Asn Val Glu Glu Met Asp | 305 | | 310 | | 315 |
| Ser Met Val Gly Lys Ile Leu Asp Ala Ile Asp Asp Phe Gly Leu Arg | 325 | | 330 | | 335 |
| Asn Asn Thr Leu Val Tyr Phe Thr Ser Asp His Gly Gly His Leu Glu | 340 | | 345 | | 350 |
| Ala Arg Arg Gly His Ala Gln Leu Gly Gly Trp Asn Gly Ile Tyr Lys | 355 | | 360 | | 365 |
| Gly Gly Lys Gly Met Gly Gly Trp Glu Gly Gly Ile Arg Val Pro Gly | 370 | | 375 | | 380 |
| Ile Val Arg Trp Pro Gly Lys Val Pro Ala Gly Arg Leu Ile Lys Glu | 385 | | 390 | | 395 |
| Pro Thr Ser Leu Met Asp Ile Leu Pro Thr Val Ala Ser Val Ser Gly | 405 | | 410 | | 415 |
| Gly Ser Leu Pro Gln Asp Arg Val Ile Asp Gly Arg Asp Leu Met Pro | 420 | | 425 | | 430 |
| Leu Leu Gln Gly Asn Val Arg His Ser Glu His Glu Phe Leu Phe His | 435 | | 440 | | 445 |
| Tyr Cys Gly Ser Tyr Leu His Ala Val Arg Trp Ile Pro Lys Asp Asp | 450 | | 455 | | 460 |
| Ser Gly Ser Val Trp Lys Ala His Tyr Val Thr Pro Val Phe Gln Pro | 465 | | 470 | | 475 |
| | | | | | 480 |

Pro Ala Ser Gly Gly Cys Tyr Val Thr Ser Leu Cys Arg Cys Phe Gly
485 490 495

Glu Gln Val Thr Tyr His Asn Pro Pro Leu Leu Phe Asp Leu Ser Arg
500 505 510

Asp Pro Ser Glu Ser Thr Pro Leu Thr Pro Ala Thr Glu Pro Leu Tyr
515 520 525

Asp Phe Val Ile Lys Lys Val Ala Asn Ala Leu Lys Glu His Gln Glu
530 535 540

Thr Ile Val Pro Val Thr Tyr Gln Leu Ser Glu Leu Asn Gln Gly Arg
545 550 555 560

Thr Trp Leu Lys Pro Cys Cys Gly Val Phe Pro Phe Cys Leu Cys Asp
565 570 575

Lys Glu Glu Glu Val Ser Gln Pro Arg Gly Pro Asn Glu Lys Arg
580 585 590

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<210> 26
<211> 1578
<212> DNA
<213> Homo sapiens
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[illegible]


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cgctgtcaag ccgcataa 1578

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<210> 27
<211> 525
<212> PRT
<213> Homo sapiens

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<400> 27

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Met Gly Trp Leu Phe Leu Lys Val Leu Leu Ala Gly Val Ser Phe Ser
1           5           10          15

```

```

Gly Phe Leu Tyr Pro Leu Val Asp Phe Cys Ile Ser Gly Lys Thr Arg
          20           25           30

```

```

Gly Gln Lys Pro Asn Phe Val Ile Ile Leu Ala Asp Asp Met Gly Trp
          35           40           45

```

```

Gly Asp Leu Gly Ala Asn Trp Ala Glu Thr Lys Asp Thr Ala Asn Leu
          50           55           60

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Asp Lys Met Ala Ser Glu Gly Met Arg Phe Val Asp Phe His Ala Ala
65 70 75 80

Ala Ser Thr Cys Ser Pro Ser Arg Ala Ser Leu Leu Thr Gly Arg Leu
85 90 95

Gly Leu Arg Asn Gly Val Thr Arg Asn Phe Ala Val Thr Ser Val Gly
100 105 110

Gly Leu Pro Leu Asn Glu Thr Thr Leu Ala Glu Val Leu Gln Gln Ala
115 120 125

Gly Tyr Val Thr Gly Ile Ile Gly Lys Trp His Leu Gly His His Gly
130 135 140

Ser Tyr His Pro Asn Phe Arg Gly Phe Asp Tyr Tyr Phe Gly Ile Pro
145 150 155 160

Tyr Ser His Asp Met Gly Cys Thr Asp Thr Pro Gly Tyr Asn His Pro
165 170 175

Pro Cys Pro Ala Cys Pro Gln Gly Asp Gly Pro Ser Arg Asn Leu Gln
180 185 190

Arg Asp Cys Tyr Thr Asp Val Ala Leu Pro Leu Tyr Glu Asn Leu Asn
195 200 205

Ile Val Glu Gln Pro Val Asn Leu Ser Ser Leu Ala Gln Lys Tyr Ala
210 215 220

Glu Lys Ala Thr Gln Phe Ile Gln Arg Ala Ser Thr Ser Gly Arg Pro
225 230 235 240

Phe Leu Leu Tyr Val Ala Leu Ala His Met His Val Pro Leu Pro Val
245 250 255

Thr Gln Leu Pro Ala Ala Pro Arg Gly Arg Ser Leu Tyr Gly Ala Gly
260 265 270

Leu Trp Glu Met Asp Ser Leu Val Gly Gln Ile Lys Asp Lys Val Asp
275 280 285

His Thr Val Lys Glu Asn Thr Phe Leu Trp Phe Thr Gly Asp Asn Gly

| 290 | 295 | 300 |
|--|-----|-----|
| Pro Trp Ala Gln Lys Cys Glu Leu Ala Gly Ser Val Gly Pro Phe Thr 305 310 315 320 | | |
| Gly Phe Trp Gln Thr Arg Gln Gly Gly Ser Pro Ala Lys Gln Thr Thr 325 330 335 | | |
| Trp Glu Gly Gly His Arg Val Pro Ala Leu Ala Tyr Trp Pro Gly Arg 340 345 350 | | |
| Val Pro Val Asn Val Thr Ser Thr Ala Leu Leu Ser Val Leu Asp Ile 355 360 365 | | |
| Phe Pro Thr Val Val Ala Leu Ala Gln Ala Ser Leu Pro Gln Gly Arg 370 375 380 | | |
| Arg Phe Asp Gly Val Asp Val Ser Glu Val Leu Phe Gly Arg Ser Gln 385 390 395 400 | | |
| Pro Gly His Arg Val Leu Phe His Pro Asn Ser Gly Ala Ala Gly Glu 405 410 415 | | |
| Phe Gly Ala Leu Gln Thr Val Arg Leu Glu Arg Tyr Lys Ala Phe Tyr 420 425 430 | | |
| Ile Thr Gly Gly Ala Arg Ala Cys Asp Gly Ser Thr Gly Pro Glu Leu 435 440 445 | | |
| Gln His Lys Phe Pro Leu Ile Phe Asn Leu Glu Asp Asp Thr Ala Glu 450 455 460 | | |
| Ala Val Pro Leu Glu Arg Gly Gly Ala Glu Tyr Gln Ala Val Leu Pro 465 470 475 480 | | |
| Glu Val Arg Lys Val Leu Ala Asp Val Leu Gln Asp Ile Ala Asn Asp 485 490 495 | | |
| Asn Ile Ser Ser Ala Asp Tyr Thr Gln Asp Pro Ser Val Thr Pro Cys 500 505 510 | | |
| Cys Asn Pro Tyr Gln Ile Ala Cys Arg Cys Gln Ala Ala 515 520 525 | | |

<210> 28
 <211> 4669
 <212> DNA
 <213> Homo sapiens

<400> 28
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 agaaaatctt caaaggacct tatctgcaga tgttctgaat acctctgaga atagagattg 420
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| Met | Lys | Tyr | Ser | Cys | Cys | Ala | Leu | Val | Leu | Ala | Val | Leu | Gly | Thr | Glu | 1 | 5 | 10 | 15 |
| Leu | Leu | Gly | Ser | Leu | Cys | Ser | Thr | Val | Arg | Ser | Pro | Arg | Phe | Arg | Gly | 20 | 25 | 30 | |
| Arg | Ile | Gln | Gln | Glu | Arg | Lys | Asn | Ile | Arg | Pro | Asn | Ile | Ile | Leu | Val | 35 | 40 | 45 | |
| Leu | Thr | Asp | Asp | Gln | Asp | Val | Glu | Leu | Gly | Ser | Leu | Gln | Val | Met | Asn | 50 | 55 | 60 | |
| Lys | Thr | Arg | Lys | Ile | Met | Glu | His | Gly | Gly | Ala | Thr | Phe | Ile | Asn | Ala | 65 | 70 | 75 | 80 |
| Phe | Val | Thr | Thr | Pro | Met | Cys | Cys | Pro | Ser | Arg | Ser | Ser | Met | Leu | Thr | 85 | 90 | 95 | |
| Gly | Lys | Tyr | Val | His | Asn | His | Asn | Val | Tyr | Thr | Asn | Asn | Glu | Asn | Cys | 100 | 105 | 110 | |
| Ser | Ser | Pro | Ser | Trp | Gln | Ala | Met | His | Glu | Pro | Arg | Thr | Phe | Ala | Val | 115 | 120 | 125 | |
| Tyr | Leu | Asn | Asn | Thr | Gly | Tyr | Arg | Thr | Ala | Phe | Phe | Gly | Lys | Tyr | Leu | 130 | 135 | 140 | |
| Asn | Glu | Tyr | Asn | Gly | Ser | Tyr | Ile | Pro | Pro | Gly | Trp | Arg | Glu | Trp | Leu | 145 | 150 | 155 | 160 |
| Gly | Leu | Ile | Lys | Asn | Ser | Arg | Phe | Tyr | Asn | Tyr | Thr | Val | Cys | Arg | Asn | 165 | 170 | 175 | |
| Gly | Ile | Lys | Glu | Lys | His | Gly | Phe | Asp | Tyr | Ala | Lys | Asp | Tyr | Phe | Thr | 180 | 185 | 190 | |
| Asp | Leu | Ile | Thr | Asn | Glu | Ser | Ile | Asn | Tyr | Phe | Lys | Met | Ser | Lys | Arg | 195 | 200 | 205 | |
| Met | Tyr | Pro | His | Arg | Pro | Val | Met | Met | Val | Ile | Ser | His | Ala | Ala | Pro | 210 | 215 | 220 | |

His Gly Pro Glu Asp Ser Ala Pro Gln Phe Ser Lys Leu Tyr Pro Asn
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Ala Ser Gln His Ile Thr Pro Ser Tyr Asn Tyr Ala Pro Asn Met Asp
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Lys His Trp Ile Met Gln Tyr Thr Gly Pro Met Leu Pro Ile His Met
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Glu Phe Thr Asn Ile Leu Gln Arg Lys Arg Leu Gln Thr Leu Met Ser
 275 280 285

Val Asp Asp Ser Val Glu Arg Leu Tyr Asn Met Leu Val Glu Thr Gly
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Glu Leu Glu Asn Thr Tyr Ile Ile Tyr Thr Ala Asp His Gly Tyr His
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Ile Gly Gln Phe Gly Leu Val Lys Gly Lys Ser Met Pro Tyr Asp Phe
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Asp Ile Arg Val Pro Phe Phe Ile Arg Gly Pro Ser Val Glu Pro Gly
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Ser Ile Val Pro Gln Ile Val Leu Asn Ile Asp Leu Ala Pro Thr Ile
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Leu Asp Ile Ala Gly Leu Asp Thr Pro Pro Asp Val Asp Gly Lys Ser
 370 375 380

Val Leu Lys Leu Leu Asp Pro Glu Lys Pro Gly Asn Arg Phe Arg Thr
 385 390 395 400

Asn Lys Lys Ala Lys Ile Trp Arg Asp Thr Phe Leu Val Glu Arg Gly
 405 410 415

Lys Phe Leu Arg Lys Lys Glu Glu Ser Ser Lys Asn Ile Gln Gln Ser
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Asn His Leu Pro Lys Tyr Glu Arg Val Lys Glu Leu Cys Gln Gln Ala
 435 440 445

Arg Tyr Gln Thr Ala Cys Glu Gln Pro Gly Gln Lys Trp Gln Cys Ile

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| Asp Leu Leu Thr Val Arg Gln Ser Thr Arg Asn Leu Tyr Ala Arg Gly | | | | |
| | 485 | | 490 | 495 |
| Phe His Asp Lys Asp Lys Glu Cys Ser Cys Arg Glu Ser Gly Tyr Arg | | | | |
| | 500 | | 505 | 510 |
| Ala Ser Arg Ser Gln Arg Lys Ser Gln Arg Gln Phe Leu Arg Asn Gln | | | | |
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| Gly Thr Pro Lys Tyr Lys Pro Arg Phe Val His Thr Arg Gln Thr Arg | | | | |
| | 530 | | 535 | 540 |
| Ser Leu Ser Val Glu Phe Glu Gly Glu Ile Tyr Asp Ile Asn Leu Glu | | | | |
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| Glu Glu Glu Glu Leu Gln Val Leu Gln Pro Arg Asn Ile Ala Lys Arg | | | | |
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| His Asp Glu Gly His Lys Gly Pro Arg Asp Leu Gln Ala Ser Ser Gly | | | | |
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| Gly Asn Arg Gly Arg Met Leu Ala Asp Ser Ser Asn Ala Val Gly Pro | | | | |
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| Pro Thr Thr Val Arg Val Thr His Lys Cys Phe Ile Leu Pro Asn Asp | | | | |
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| Ser Ile His Cys Glu Arg Glu Leu Tyr Gln Ser Ala Arg Ala Trp Lys | | | | |
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| Asp His Lys Ala Tyr Ile Asp Lys Glu Ile Glu Ala Leu Gln Asp Lys | | | | |
| | 645 | | 650 | 655 |
| Ile Lys Asn Leu Arg Glu Val Arg Gly His Leu Lys Arg Arg Lys Pro | | | | |
| | 660 | | 665 | 670 |
| Glu Glu Cys Ser Cys Ser Lys Gln Ser Tyr Tyr Asn Lys Glu Lys Gly | | | | |
| | 675 | | 680 | 685 |

Val Lys Lys Gln Glu Lys Leu Lys Ser His Leu His Pro Phe Lys Glu
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Ala Ala Gln Glu Val Asp Ser Lys Leu Gln Leu Phe Lys Glu Asn Asn
 705 710 715 720

Arg Arg Arg Lys Lys Glu Arg Lys Glu Lys Arg Arg Gln Arg Lys Gly
 725 730 735

Glu Glu Cys Ser Leu Pro Gly Leu Thr Cys Phe Thr His Asp Asn Asn
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His Trp Gln Thr Ala Pro Phe Trp Asn Leu Gly Ser Phe Cys Ala Cys
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Thr Ser Ser Asn Asn Asn Thr Tyr Trp Cys Leu Arg Thr Val Asn Glu
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Thr His Asn Phe Leu Phe Cys Glu Phe Ala Thr Gly Phe Leu Glu Tyr
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Phe Asp Met Asn Thr Asp Pro Tyr Gln Leu Thr Asn Thr Val His Thr
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Val Glu Arg Gly Ile Leu Asn Gln Leu His Val Gln Leu Met Glu Leu
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Arg Ser Cys Gln Gly Tyr Lys Gln Cys Asn Pro Arg Pro Lys Asn Leu
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| ggcagtcgag | tgtttgcaga | ccggggcgag | tcctgtgaaa | gcagataaaa | gaaaacattt | 240 |
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Gly Arg Phe Gln Arg Asp Arg Arg Asn Ile Arg Pro Asn Ile Ile Leu
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Val Leu Thr Asp Asp Gln Asp Val Glu Leu Gly Ser Met Gln Val Met
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Asn Lys Thr Arg Arg Ile Met Glu Gln Gly Gly Ala His Phe Ile Asn
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Ala Phe Val Thr Thr Pro Met Cys Cys Pro Ser Arg Ser Ser Ile Leu
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Thr Gly Lys Tyr Val His Asn His Asn Thr Tyr Thr Asn Asn Glu Asn
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Cys Ser Ser Pro Ser Trp Gln Ala Gln His Glu Ser Arg Thr Phe Ala
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Val Tyr Leu Asn Ser Thr Gly Tyr Arg Thr Ala Phe Phe Gly Lys Tyr
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Leu Asn Glu Tyr Asn Gly Ser Tyr Val Pro Pro Gly Trp Lys Glu Trp
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Val Gly Leu Leu Lys Asn Ser Arg Phe Tyr Asn Tyr Thr Leu Cys Arg
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Asn Gly Val Lys Glu Lys His Gly Ser Asp Tyr Ser Lys Asp Tyr Leu
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Thr Asp Leu Ile Thr Asn Asp Ser Val Ser Phe Phe Arg Thr Ser Lys
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Lys Met Tyr Pro His Arg Pro Val Leu Met Val Ile Ser His Ala Ala
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Pro His Gly Pro Glu Asp Ser Ala Pro Gln Tyr Ser Arg Leu Phe Pro
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Asn Ala Ser Gln His Ile Thr Pro Ser Tyr Asn Tyr Ala Pro Asn Pro
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Asp Lys His Trp Ile Met Arg Tyr Thr Gly Pro Met Lys Pro Ile His
260 265 270

Met Glu Phe Thr Asn Met Leu Gln Arg Lys Arg Leu Gln Thr Leu Met
275 280 285

Ser Val Asp Asp Ser Met Glu Thr Ile Tyr Asn Met Leu Val Glu Thr
290 295 300

Gly Glu Leu Asp Asn Thr Tyr Ile Val Tyr Thr Ala Asp His Gly Tyr

| | | | | | | |
|---|--|-----|--|-----|--|-----|
| 305 | | 310 | | 315 | | 320 |
| His Ile Gly Gln Phe Gly Leu Val Lys Gly Lys Ser Met Pro Tyr Glu | | | | | | |
| | | 325 | | 330 | | 335 |
| Phe Asp Ile Arg Val Pro Phe Tyr Val Arg Gly Pro Asn Val Glu Ala | | | | | | |
| | | 340 | | 345 | | 350 |
| Gly Cys Leu Asn Pro His Ile Val Leu Asn Ile Asp Leu Ala Pro Thr | | | | | | |
| | | 355 | | 360 | | 365 |
| Ile Leu Asp Ile Ala Gly Leu Asp Ile Pro Ala Asp Met Asp Gly Lys | | | | | | |
| | | 370 | | 375 | | 380 |
| Ser Ile Leu Lys Leu Leu Asp Thr Glu Arg Pro Val Asn Arg Phe His | | | | | | |
| | | 385 | | 390 | | 395 |
| Leu Lys Lys Lys Met Arg Val Trp Arg Asp Ser Phe Leu Val Glu Arg | | | | | | |
| | | 405 | | 410 | | 415 |
| Gly Lys Leu Leu His Lys Arg Asp Asn Asp Lys Val Asp Ala Gln Glu | | | | | | |
| | | 420 | | 425 | | 430 |
| Glu Asn Phe Leu Pro Lys Tyr Gln Arg Val Lys Asp Leu Cys Gln Arg | | | | | | |
| | | 435 | | 440 | | 445 |
| Ala Glu Tyr Gln Thr Ala Cys Glu Gln Leu Gly Gln Lys Trp Gln Cys | | | | | | |
| | | 450 | | 455 | | 460 |
| Val Glu Asp Ala Thr Gly Lys Leu Lys Leu His Lys Cys Lys Gly Pro | | | | | | |
| | | 465 | | 470 | | 475 |
| Met Arg Leu Gly Gly Ser Arg Ala Leu Ser Asn Leu Val Pro Lys Tyr | | | | | | |
| | | 485 | | 490 | | 495 |
| Tyr Gly Gln Gly Ser Glu Ala Cys Thr Cys Asp Ser Gly Asp Tyr Lys | | | | | | |
| | | 500 | | 505 | | 510 |
| Leu Ser Leu Ala Gly Arg Arg Lys Lys Leu Phe Lys Lys Lys Tyr Lys | | | | | | |
| | | 515 | | 520 | | 525 |
| Ala Ser Tyr Val Arg Ser Arg Ser Ile Arg Ser Val Ala Ile Glu Val | | | | | | |
| | | 530 | | 535 | | 540 |

Asp Gly Arg Val Tyr His Val Gly Leu Gly Asp Ala Ala Gln Pro Arg
 545 550 555 560

Asn Leu Thr Lys Arg His Trp Pro Gly Ala Pro Glu Asp Gln Asp Asp
 565 570 575

Lys Asp Gly Gly Asp Phe Ser Gly Thr Gly Gly Leu Pro Asp Tyr Ser
 580 585 590

Ala Ala Asn Pro Ile Lys Val Thr His Arg Cys Tyr Ile Leu Glu Asn
 595 600 605

Asp Thr Val Gln Cys Asp Leu Asp Leu Tyr Lys Ser Leu Gln Ala Trp
 610 615 620

Lys Asp His Lys Leu His Ile Asp His Glu Ile Glu Thr Leu Gln Asn
 625 630 635 640

Lys Ile Lys Asn Leu Arg Glu Val Arg Gly His Leu Lys Lys Lys Arg
 645 650 655

Pro Glu Glu Cys Asp Cys His Lys Ile Ser Tyr His Thr Gln His Lys
 660 665 670

Gly Arg Leu Lys His Arg Gly Ser Ser Leu His Pro Phe Arg Lys Gly
 675 680 685

Leu Gln Glu Lys Asp Lys Val Trp Leu Leu Arg Glu Gln Lys Arg Lys
 690 695 700

Lys Lys Leu Arg Lys Leu Leu Lys Arg Leu Gln Asn Asn Asp Thr Cys
 705 710 715 720

Ser Met Pro Gly Leu Thr Cys Phe Thr His Asp Asn Gln His Trp Gln
 725 730 735

Thr Ala Pro Phe Trp Thr Leu Gly Pro Phe Cys Ala Cys Thr Ser Ala
 740 745 750

Asn Asn Asn Thr Tyr Trp Cys Met Arg Thr Ile Asn Glu Thr His Asn
 755 760 765

Phe Leu Phe Cys Glu Phe Ala Thr Gly Phe Leu Glu Tyr Phe Asp Leu
 770 775 780

Asn Thr Asp Pro Tyr Gln Leu Met Asn Ala Val Asn Thr Leu Asp Arg
 785 790 795 800

Asp Val Leu Asn Gln Leu His Val Gln Leu Met Glu Leu Arg Ser Cys
 805 810 815

Lys Gly Tyr Lys Gln Cys Asn Pro Arg Thr Arg Asn Met Asp Leu Gly
 820 825 830

Leu Lys Asp Gly Gly Ser Tyr Glu Gln Tyr Arg Gln Phe Gln Arg Arg
 835 840 845

Lys Trp Pro Glu Met Lys Arg Pro Ser Ser Lys Ser Leu Gly Gln Leu
 850 855 860

Trp Glu Gly Trp Glu Gly
 865 870

<210> 32
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Consensus sequence

<220>
 <221> VARIANT
 <222> 1
 <223> Leu or Val

<220>
 <221> VARIANT
 <222> 2
 <223> Cys or Ser

<220>
 <221> misc_feature
 <222> 3
 <223> Xaa can be any naturally occurring amino acid

<400> 32

Xaa Xaa Xaa Pro Ser Arg
 1 5

<210> 33
 <211> 23
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Sequence derived from human Arylsulfatase A

<400> 33

Met Thr Asp Phe Tyr Val Pro Val Ser Leu Cys Thr Pro Ser Arg Ala
 1 5 10 15

Ala Leu Leu Thr Gly Arg Ser
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<210> 34
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> a variant of the ASA65-80 peptide, in which residues Cys69, Pro71
 and Arg73, critical for FGly formation, were scrambled

<400> 34

Pro Val Ser Leu Pro Thr Arg Ser Cys Ala Ala Leu Leu Thr Gly Arg
 1 5 10 15

<210> 35
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> a variant of the ASA65-80 peptide, in which the Cys69 was
 replaced by a Serine

<400> 35

Pro Val Ser Leu Ser Thr Pro Ser Arg Ala Ala Leu Leu Thr Gly Arg
 1 5 10 15

<210> 36
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> human FGE-specific PCR primer

<400> 36
ccaatgtagg tcagacacg 19

<210> 37
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> human FGE-specific PCR primer

<400> 37
acatggcccg cgggac 16

<210> 38
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> human FGE-specific PCR primer

<400> 38
cgactgctcc ttggactgg 19

<210> 39
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> human FGE-specific PCR primer

<400> 39
ggaattcggg acaacatggc tgcg 24

<210> 40
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> HA-specific primer

<400> 40
cccaagctta tgcgtagtca ggcacatcat acggatagtc catggtgggc aggc 54

<210> 41
<211> 57
<212> DNA
<213> Artificial Sequence

<220>

<223> c-myc -specific primer

<400> 41

cccaagctta caggtcttct tcagaaatca gcttttggtc gtccatggtg ggcaggc 57

<210> 42

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> RGS-His6 - specific primer

<400> 42

cccaagctta gtgatggtga tggatgatgcg atcctctgtc catggtgggc aggc 54

<210> 43

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> tryptic oligopeptide from a human FGE preparation

<400> 43

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Gln | Asn | Thr | Pro | Asp | Ser | Ser | Ala | Ser | Asn | Leu | Gly | Phe | Arg |
| 1 | | | | 5 | | | | 10 | | | | | 15 | |

<210> 44

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> tryptic oligopeptide from a human FGE preparation

<220>

<221> MISC_FEATURE

<222> (1)..(19)

<223> tryptic oligopeptide from a human FGE preparation

<400> 44

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Pro | Ile | Pro | Ala | Gly | Val | Phe | Thr | Met | Gly | Thr | Asp | Asp | Pro |
| 1 | | | | 5 | | | | 10 | | | | | 15 | | |

Gln Ile Lys

<210> 45
 <211> 906
 <212> DNA
 <213> Homo sapiens

<400> 45
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 aagctaggaa atggacaggc tactagcatg gtccaactgc aggggtgggag attcctgatg 120
 ggaacaaatt ctccagacag cagagatggt gaagggcctg tgcgggaggc gacagtgaaa 180
 ccctttgcc tgcacatatt tcctgtcacc aacaaagatt tcagggattt tgtcagggag 240
 aaaaagtatc ggacagaagc tgagatgttt ggatggagct ttgtctttga ggactttgtc 300
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 gagcaccag tgttacacgt gagctggaat gacgcccgtg cctactgtgc ttggcgggga 480
 aaacgactgc ccacggagga agagtgggag tttgccgcc gagggggctt gaaggggtcaa 540
 gtttaccat gggggaactg gttccagcca aaccgcacca acctgtggca gggaaagttc 600
 cccaaggag acaaagctga ggatggcttc catggagtct cccagtga tgccttcccc 660
 gccagaaca actacgggct ctatgacctc ctggggaacg tgtgggagtg gacagcatca 720
 ccgtaccagg ctgctgagca ggacatgcgc gtcctccggg gggcatcctg gatcgacaca 780
 gctgatggct ctgccaatca ccgggcccgg gtcaccacca ggatgggcaa cactccagat 840
 tcagcctcag acaacctcgg tttccgctgt gctgcagacg caggccggcc gccaggggag 900
 ctgtaa 906

<210> 46
 <211> 301
 <212> PRT
 <213> Homo sapiens

<400> 46

Met Ala Arg His Gly Leu Pro Leu Leu Pro Leu Leu Ser Leu Leu Val
 1 5 10 15

Gly Ala Trp Leu Lys Leu Gly Asn Gly Gln Ala Thr Ser Met Val Gln
 20 25 30

Leu Gln Gly Gly Arg Phe Leu Met Gly Thr Asn Ser Pro Asp Ser Arg
 35 40 45

Asp Gly Glu Gly Pro Val Arg Glu Ala Thr Val Lys Pro Phe Ala Ile
50 55 60

Asp Ile Phe Pro Val Thr Asn Lys Asp Phe Arg Asp Phe Val Arg Glu
65 70 75 80

Lys Lys Tyr Arg Thr Glu Ala Glu Met Phe Gly Trp Ser Phe Val Phe
85 90 95

Glu Asp Phe Val Ser Asp Glu Leu Arg Asn Lys Ala Thr Gln Pro Met
100 105 110

Lys Ser Val Leu Trp Trp Leu Pro Val Glu Lys Ala Phe Trp Arg Gln
115 120 125

Pro Ala Gly Pro Gly Ser Gly Ile Arg Glu Arg Leu Glu His Pro Val
130 135 140

Leu His Val Ser Trp Asn Asp Ala Arg Ala Tyr Cys Ala Trp Arg Gly
145 150 155 160

Lys Arg Leu Pro Thr Glu Glu Glu Trp Glu Phe Ala Ala Arg Gly Gly
165 170 175

Leu Lys Gly Gln Val Tyr Pro Trp Gly Asn Trp Phe Gln Pro Asn Arg
180 185 190

Thr Asn Leu Trp Gln Gly Lys Phe Pro Lys Gly Asp Lys Ala Glu Asp
195 200 205

Gly Phe His Gly Val Ser Pro Val Asn Ala Phe Pro Ala Gln Asn Asn
210 215 220

Tyr Gly Leu Tyr Asp Leu Leu Gly Asn Val Trp Glu Trp Thr Ala Ser
225 230 235 240

Pro Tyr Gln Ala Ala Glu Gln Asp Met Arg Val Leu Arg Gly Ala Ser
245 250 255

Trp Ile Asp Thr Ala Asp Gly Ser Ala Asn His Arg Ala Arg Val Thr
260 265 270

Thr Arg Met Gly Asn Thr Pro Asp Ser Ala Ser Asp Asn Leu Gly Phe
 275 280 285

Arg Cys Ala Ala Asp Ala Gly Arg Pro Pro Gly Glu Leu
 290 295 300

<210> 47
 <211> 927
 <212> DNA
 <213> Mus musculus

<400> 47
 atgcgctctg agttcttggtt cccagcatg ggcttccttgc tccctccggt gttgctgctg 60
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 ctgccagggt gccggtttct gatggggaca gacgctccag atggcagaga cgggtgaagg 180
 cctgccccgg aagtgcagct aaaacccttt gccatcgaca tatttccagt caccaataaa 240
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 aacttatggc agggaaagtt ccccaaaggt gacaaagctg aagatggttt tcatggactg 660
 tcaccagtga acgctttccc cccacagaac aactacggac tgtatgacct catgggcaat 720
 gtgtgggagt ggacagcgtc cacataccta cctgctggcc aggacatgct tgcctccgg 780
 ggggcatcat ggatcgacac cgcagacggc tctgctaata acagggctcg ggtcaccacc 840
 aggatgggaa aactccaga ctcagcctca gacaacctgg gcttccgctg cgcctccagt 900
 gcaggccgac cgaaggagga cctgtga 927

<210> 48
 <211> 308
 <212> PRT
 <213> Mus musculus

<400> 48

Met Arg Ser Glu Phe Trp Phe Pro Ser Met Gly Ser Leu Leu Pro Pro
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Val Leu Leu Leu Arg Leu Leu Ser Cys Pro Arg Leu Gln Leu Gly His
 20 25 30

Ala Gln Asp Pro Ala Met Val His Leu Pro Gly Gly Arg Phe Leu Met
 35 40 45

Gly Thr Asp Ala Pro Asp Gly Arg Asp Gly Glu Gly Pro Ala Arg Glu
 50 55 60

Val Thr Val Lys Pro Phe Ala Ile Asp Ile Phe Pro Val Thr Asn Lys
 65 70 75 80

Asp Phe Arg Glu Phe Val Arg Glu Lys Lys Tyr Gln Thr Glu Ala Glu
 85 90 95

Ala Phe Gly Trp Ser Phe Val Phe Glu Asp Phe Val Ser Pro Glu Leu
 100 105 110

Arg Lys Gln Glu Asn Leu Met Pro Ala Val His Trp Trp Gln Pro Val
 115 120 125

Pro Lys Ala Phe Trp Arg Gln Pro Ala Gly Pro Gly Ser Gly Ile Arg
 130 135 140

Glu Lys Leu Glu Leu Pro Val Val His Val Ser Trp Asn Asp Ala Gly
 145 150 155 160

Ala Tyr Cys Ala Trp Arg Gly Arg Arg Leu Pro Thr Glu Glu Glu Trp
 165 170 175

Glu Phe Ala Ala Arg Gly Gly Leu Lys Gly Gln Val Tyr Pro Trp Gly
 180 185 190

Asn Arg Phe Gln Pro Asn Arg Thr Asn Leu Trp Gln Gly Lys Phe Pro
 195 200 205

Lys Gly Asp Lys Ala Glu Asp Gly Phe His Gly Leu Ser Pro Val Asn
 210 215 220

Ala Phe Pro Pro Gln Asn Asn Tyr Gly Leu Tyr Asp Leu Met Gly Asn
 225 230 235 240

Val Trp Glu Trp Thr Ala Ser Thr Tyr Gln Pro Ala Gly Gln Asp Met
 245 250 255

Arg Val Leu Arg Gly Ala Ser Trp Ile Asp Thr Ala Asp Gly Ser Ala
 260 265 270

Asn His Arg Ala Arg Val Thr Thr Arg Met Gly Asn Thr Pro Asp Ser
 275 280 285

Ala Ser Asp Asn Leu Gly Phe Arg Cys Ala Ser Ser Ala Gly Arg Pro
 290 295 300

Lys Glu Asp Leu
 305

<210> 49
 <211> 855
 <212> DNA
 <213> Mus musculus

<400> 49
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 gtcagcaatg cggattttga gaagtttggtg aactcgactg gctatttgac agaggctgag 180
 aagtttgagg actctttcgt ctttgaaggc atgttgagcg agcaagtga aacgcataac 240
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 ccagagggtc cggactccag tattctgcac aggtcaaata atccggttct ccatgtttcc 360
 tggaacgatg ctgttgccca ctgcacatgg gcgggcaaga ggttgccctac tgaggcagag 420
 tgggaataca gctgtagagg aggctgcag aacaggcttt tcccctgggg caacaaactg 480
 cagcccaaag gacagcatta tgccaacatc tggcagggca agtttcctgt gagcaacact 540
 ggcgaggatg gcttccaagg aactgcccc gttgatgcct ttcctccaa tggctatggc 600
 ttatacaaca tagtggggaa tgtgtgggag tggacctcag actggtggac tgttcacat 660
 tctgttgagg aaacgttcaa cccaaagggc cccacttctg ggaaagaccg agtgaagaag 720
 ggtggatcct acatgtgcca taagtcctat tgctataggt accgctgtgc agctcgaagc 780
 cagaacacac cagatagctc tgcacccaac ctgggattcc gatgtgcagc cgaccacctg 840
 cccaccgcag actga 855

<210> 50
 <211> 284
 <212> PRT
 <213> Mus musculus

<400> 50

Met Val Pro Ile Pro Ala Gly Val Phe Thr Met Gly Thr Asp Asp Pro
 1 5 10 15

Gln Ile Arg Gln Asp Gly Glu Ala Pro Ala Arg Arg Val Thr Val Asp
 20 25 30

Gly Phe Tyr Met Asp Ala Tyr Glu Val Ser Asn Ala Asp Phe Glu Lys
 35 40 45

Phe Val Asn Ser Thr Gly Tyr Leu Thr Glu Ala Glu Lys Phe Gly Asp
 50 55 60

Ser Phe Val Phe Glu Gly Met Leu Ser Glu Gln Val Lys Thr His Ile
 65 70 75 80

His Gln Ala Val Ala Ala Ala Pro Trp Trp Leu Pro Val Lys Gly Ala
 85 90 95

Asn Trp Arg His Pro Glu Gly Pro Asp Ser Ser Ile Leu His Arg Ser
 100 105 110

Asn His Pro Val Leu His Val Ser Trp Asn Asp Ala Val Ala Tyr Cys
 115 120 125

Thr Trp Ala Gly Lys Arg Leu Pro Thr Glu Ala Glu Trp Glu Tyr Ser
 130 135 140

Cys Arg Gly Gly Leu Gln Asn Arg Leu Phe Pro Trp Gly Asn Lys Leu
 145 150 155 160

Gln Pro Lys Gly Gln His Tyr Ala Asn Ile Trp Gln Gly Lys Phe Pro
 165 170 175

Val Ser Asn Thr Gly Glu Asp Gly Phe Gln Gly Thr Ala Pro Val Asp
 180 185 190

Ala Phe Pro Pro Asn Gly Tyr Gly Leu Tyr Asn Ile Val Gly Asn Val

195

200

205

Trp Glu Trp Thr Ser Asp Trp Trp Thr Val His His Ser Val Glu Glu
 210 215 220

Thr Phe Asn Pro Lys Gly Pro Thr Ser Gly Lys Asp Arg Val Lys Lys
 225 230 235 240

Gly Gly Ser Tyr Met Cys His Lys Ser Tyr Cys Tyr Arg Tyr Arg Cys
 245 250 255

Ala Ala Arg Ser Gln Asn Thr Pro Asp Ser Ser Ala Ser Asn Leu Gly
 260 265 270

Phe Arg Cys Ala Ala Asp His Leu Pro Thr Ala Asp
 275 280

<210> 51

<211> 1011

<212> DNA

<213> *Drosophila melanogaster*

<400> 51

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gtgtgccagc aacgagcaca ggggtgcacac agccactacc gggattacta tggcgaactg      180
gagccaaata ttgcggacat gtcactgctt cggggaggca cggtttacat ggggtactgac      240
aaaccgcact ttccggccga ccgcgaggct ccggaacggc aggtgaagct gaatgacttc      300
tacatcgaca agtatgaggt ttccaacgaa gcctttgcga agtttgttct gcacactaac      360
tacaccacgg aggctgagcg atatggcgac agttttctgt ttaagagcct tttgagccca      420
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gactttcccg atggcaacct ggctgaagat gggtttgagt acaccagccc cgtggatgcc      780
ttccgacaga atatttacga cctgcacaac atggtgggca acgtctggga gtggacggca      840

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gatctgtggg acgtaaatga cgtttagcgat aatccaaatc gggtaagaa gggcggttct 900
 tatctgtgtc acaagtccta ctgctacagg tacaggtgcg cggcacgctc gcagaacaca 960
 gaagacagtt cagccggtaa cctggggtttt cgggtgcgcca agaatgcgtg a 1011

<210> 52
 <211> 336
 <212> PRT
 <213> *Drosophila melanogaster*

<400> 52

Met Thr Thr Ile Ile Leu Val Leu Phe Ile Trp Ile Val Leu Phe Asn
 1 5 10 15

Asp Val Ser Ser Asp Cys Gly Cys Gln Lys Leu Asp Arg Lys Ala Pro
 20 25 30

Asp Met Pro Ser Ile Ser Gly Gln Val Cys Gln Gln Arg Ala Gln Gly
 35 40 45

Ala His Ser His Tyr Arg Asp Tyr Tyr Gly Glu Leu Glu Pro Asn Ile
 50 55 60

Ala Asp Met Ser Leu Leu Pro Gly Gly Thr Val Tyr Met Gly Thr Asp
 65 70 75 80

Lys Pro His Phe Pro Ala Asp Arg Glu Ala Pro Glu Arg Gln Val Lys
 85 90 95

Leu Asn Asp Phe Tyr Ile Asp Lys Tyr Glu Val Ser Asn Glu Ala Phe
 100 105 110

Ala Lys Phe Val Leu His Thr Asn Tyr Thr Thr Glu Ala Glu Arg Tyr
 115 120 125

Gly Asp Ser Phe Leu Phe Lys Ser Leu Leu Ser Pro Leu Glu Gln Lys
 130 135 140

Asn Leu Glu Asp Phe Arg Val Ala Ser Ala Val Trp Trp Tyr Lys Val
 145 150 155 160

Ala Gly Val Asn Trp Arg His Pro Asn Gly Val Asp Ser Asp Ile Asp
 165 170 175

His Leu Gly Arg His Pro Val Val His Val Ser Trp Arg Asp Ala Val
 180 185 190

Glu Tyr Cys Lys Trp Ala Gly Lys Arg Leu Pro Ser Glu Ala Glu Trp
 195 200 205

Glu Ala Ala Cys Arg Gly Gly Lys Glu Arg Lys Leu Phe Pro Trp Gly
 210 215 220

Asn Lys Leu Met Pro Arg Asn Glu His Trp Leu Asn Ile Trp Gln Gly
 225 230 235 240

Asp Phe Pro Asp Gly Asn Leu Ala Glu Asp Gly Phe Glu Tyr Thr Ser
 245 250 255

Pro Val Asp Ala Phe Arg Gln Asn Ile Tyr Asp Leu His Asn Met Val
 260 265 270

Gly Asn Val Trp Glu Trp Thr Ala Asp Leu Trp Asp Val Asn Asp Val
 275 280 285

Ser Asp Asn Pro Asn Arg Val Lys Lys Gly Gly Ser Tyr Leu Cys His
 290 295 300

Lys Ser Tyr Cys Tyr Arg Tyr Arg Cys Ala Ala Arg Ser Gln Asn Thr
 305 310 315 320

Glu Asp Ser Ser Ala Gly Asn Leu Gly Phe Arg Cys Ala Lys Asn Ala
 325 330 335

<210> 53
 <211> 870
 <212> DNA
 <213> Anopheles gambiae

<400> 53
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 ccggccccggc ccgcgacgat ccgcgacttt tacctcgacc agtacgaagt ctccaacgca 180
 cagttcaagg cattcgtcga ccagacgggc tacgtcacgg aggcggaaaa gtttggcgac 240
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gtggcggcgg cgccctggtg gtacaaggta cgtggagcct cctggcagca tccggaaggt 360
 gatgtgtcac gtgatataag cgaccgattg gaccatccgg tggcgcacgt gtccctggaac 420
 gatgcggtcg cgtactgctc ctggaaaggg aagcgctgc cgacggaagc ggaatgggaa 480
 gcggcctgcc ggggcggtcg caagcagaag ctgttcccct ggggtaacaa gctgatgccg 540
 aaggagcagc acatgatgaa catatggcag ggcgagttcc cggacagcaa tctgaaggag 600
 gatggctacg agaccacctg cccggtgacg tccttcgcc agaaccggtt cgagctgtac 660
 aacatcggtg gcaacgtgtg ggagtggacg gcggatcttt gggacgcgaa ggatgcggcc 720
 atcgagcgca agccgggcag cgatccaccg aatcgggtga aaaagggtgg ctcatacctg 780
 tgtcacgaat cgtactgcta tcgctatcgc tgtgcggctc gatcgagaa caccgaggac 840
 agttcggcgg gcaatctggg cttccggtgc 870

<210> 54
 <211> 290
 <212> PRT
 <213> *Anopheles gambiae*

<400> 54

Pro Glu Ser Leu Leu Asp Leu Val Glu His Ser Lys Arg Phe Glu Asp
 1 5 10 15

Met Ser Leu Ile Pro Gly Gly Glu Tyr Val Ile Gly Thr Asn Glu Pro
 20 25 30

Ile Phe Val Lys Asp Arg Glu Ser Pro Ala Arg Pro Ala Thr Ile Arg
 35 40 45

Asp Phe Tyr Leu Asp Gln Tyr Glu Val Ser Asn Ala Gln Phe Lys Ala
 50 55 60

Phe Val Asp Gln Thr Gly Tyr Val Thr Glu Ala Glu Lys Phe Gly Asp
 65 70 75 80

Ser Phe Val Phe Gln Gln Leu Leu Ser Glu Pro Val Arg Gln Gln Tyr
 85 90 95

Glu Asp Phe Arg Val Ala Ala Ala Pro Trp Trp Tyr Lys Val Arg Gly
 100 105 110

Ala Ser Trp Gln His Pro Glu Gly Asp Val Ser Arg Asp Ile Ser Asp

115

120

125

Arg Leu Asp His Pro Val Val His Val Ser Trp Asn Asp Ala Val Ala
 130 135 140

Tyr Cys Ala Trp Lys Gly Lys Arg Leu Pro Thr Glu Ala Glu Trp Glu
 145 150 155 160

Ala Ala Cys Arg Gly Gly Arg Lys Gln Lys Leu Phe Pro Trp Gly Asn
 165 170 175

Lys Leu Met Pro Lys Glu Gln His Met Met Asn Ile Trp Gln Gly Glu
 180 185 190

Phe Pro Asp Ser Asn Leu Lys Glu Asp Gly Tyr Glu Thr Thr Cys Pro
 195 200 205

Val Thr Ser Phe Arg Gln Asn Pro Phe Glu Leu Tyr Asn Ile Val Gly
 210 215 220

Asn Val Trp Glu Trp Thr Ala Asp Leu Trp Asp Ala Lys Asp Ala Ala
 225 230 235 240

Ile Glu Arg Lys Pro Gly Ser Asp Pro Pro Asn Arg Val Lys Lys Gly
 245 250 255

Gly Ser Tyr Leu Cys His Glu Ser Tyr Cys Tyr Arg Tyr Arg Cys Ala
 260 265 270

Ala Arg Ser Gln Asn Thr Glu Asp Ser Ser Ala Gly Asn Leu Gly Phe
 275 280 285

Arg Cys
 290

<210> 55

<211> 945

<212> DNA

<213> Streptomyces coelicolor

<400> 55

gtggcgcgtgg ccgccccgtc ccccgcggcc gccgcggagc cggggcccgcc cgcccgctccg 60

cgctcgaccc gcggacaggt gcgcctgccg ggcggtgagt tcgcgatggg ggacgccttc 120

```

ggggagggat atccggccga cggcgagaca cccgtgcaca cggtgcgctt gcggcccttc 180
cacatcgacg agaccgccgt caccaacgcc cggttcgccg ccttcgtcaa ggcgaccggc 240
catgtgaccg acgccgaacg cttcggctcc tcggccgtct tccacctggt cgtcgccgcc 300
ccggacgccg acgtcctcgg cagcgccgcc ggcgccccct ggtggatcaa cgtgcggggc 360
gcccactggc gccgccccga gggcgcccg cccgacatca ccggccggcc gaaccatccg 420
gtcgtccacg tctcctggaa cgatgccacc gcctacgcgc ggtgggcccg caagcgctg 480
cccaccgagg ccgaatggga gtacgccgcc cgcgggggac tggccggccg ccgctacgcc 540
tggggcgacg agctgacccc gggcgggccg tggcgctgca acatctggca gggccgcttc 600
ccgcacgtca acacggccga ggacgggcac ctgagcaccg caccggtcaa gtcctaccgg 660
cccaacggcc acggcctgtg gaacaccgcy ggcaacgtgt gggaatggtg ctccgactgg 720
ttctcgccca cctactacgc cgaatcacc accgtcgacc cgcacggccc cgggaccggg 780
gcggcacggg tgctgcgcgg cggctcctac ctgtgccacg actcctactg caaccgctac 840
cgggtcgccg cccgctcctc caacaccccg gactcctcgt ccggcaacct cggattccgc 900
tgcgccaacg acgcggaact cagtcggga tcagccgctg agtga 945

```

<210> 56

<211> 314

<212> PRT

<213> Streptomyces coelicolor

<400> 56

```

Met Ala Val Ala Ala Pro Ser Pro Ala Ala Ala Ala Glu Pro Gly Pro
1           5           10          15

```

```

Ala Ala Arg Pro Arg Ser Thr Arg Gly Gln Val Arg Leu Pro Gly Gly
          20          25          30

```

```

Glu Phe Ala Met Gly Asp Ala Phe Gly Glu Gly Tyr Pro Ala Asp Gly
          35          40          45

```

```

Glu Thr Pro Val His Thr Val Arg Leu Arg Pro Phe His Ile Asp Glu
          50          55          60

```

```

Thr Ala Val Thr Asn Ala Arg Phe Ala Ala Phe Val Lys Ala Thr Gly
65          70          75          80

```

```

His Val Thr Asp Ala Glu Arg Phe Gly Ser Ser Ala Val Phe His Leu

```


85

90

95

Val Val Ala Ala Pro Asp Ala Asp Val Leu Gly Ser Ala Ala Gly Ala
 100 105 110

Pro Trp Trp Ile Asn Val Arg Gly Ala His Trp Arg Arg Pro Glu Gly
 115 120 125

Ala Arg Ser Asp Ile Thr Gly Arg Pro Asn His Pro Val Val His Val
 130 135 140

Ser Trp Asn Asp Ala Thr Ala Tyr Ala Arg Trp Ala Gly Lys Arg Leu
 145 150 155 160

Pro Thr Glu Ala Glu Trp Glu Tyr Ala Ala Arg Gly Gly Leu Ala Gly
 165 170 175

Arg Arg Tyr Ala Trp Gly Asp Glu Leu Thr Pro Gly Gly Arg Trp Arg
 180 185 190

Cys Asn Ile Trp Gln Gly Arg Phe Pro His Val Asn Thr Ala Glu Asp
 195 200 205

Gly His Leu Ser Thr Ala Pro Val Lys Ser Tyr Arg Pro Asn Gly His
 210 215 220

Gly Leu Trp Asn Thr Ala Gly Asn Val Trp Glu Trp Cys Ser Asp Trp
 225 230 235 240

Phe Ser Pro Thr Tyr Tyr Ala Glu Ser Pro Thr Val Asp Pro His Gly
 245 250 255

Pro Gly Thr Gly Ala Ala Arg Val Leu Arg Gly Gly Ser Tyr Leu Cys
 260 265 270

His Asp Ser Tyr Cys Asn Arg Tyr Arg Val Ala Ala Arg Ser Ser Asn
 275 280 285

Thr Pro Asp Ser Ser Ser Gly Asn Leu Gly Phe Arg Cys Ala Asn Asp
 290 295 300

Ala Asp Leu Thr Ser Gly Ser Ala Ala Glu
 305 310

<210> 57
 <211> 1005
 <212> DNA
 <213> *Corynebacterium efficiens*

<400> 57
 gtggttcgcc atcgactggg ccaccggccc tgcacactga ggattacgtc catgagtaac 60
 tgctgctccc cgtcaagcgc acaatggcgt accactaccc gggatttata agatcctgtc 120
 aatcccacca ctccatgcaa cccggaacaa tcccgcgatg ctgtgacact gccgggtgga 180
 gctttccaca tgggcgatca tcacggggag gggatcccg cggacgggga ggggccagta 240
 catgaggttc acctcgcccc cttcggcatt aatgtcacca cggtcacgaa tgccgagttc 300
 ggacgattta ttgaagccac agggatatac acgacagcgg aacgctacgg tgtctcggct 360
 gtattctacg cagcgttcca agggcaacgc gctgacattc ttcgccaggt tcccggcgtg 420
 ccctggtggc tggcgggtcaa ggggtgcgaac tggcagcgtc ccaacggccc cggatccacc 480
 ctggacgggc ttgaggacca ccccgctcgtt cacgtttcct gggatgatgc cgttgccctac 540
 tgcacctggg ctggcgggtc tctgcccacc gaagccgagt ggggaatacgc cggccggggt 600
 ggactgcagg gcgcacgata tgcttggggg gataacctcg ccctagacgg gaggtggaac 660
 tgcaatatct ggcagggggg ctcccccatg gagaacaccg ccgcggatgg ttacctcacc 720
 actgcaccgg tgaagacctc cacgcccatt ggatacggtc tgtggcagat ggcagggaat 780
 gtatgggaat ggtgccagga ctggtttgat gcggagtact actcccgtgc ttctccatc 840
 aaccgcggg gaccggatac cgggtgcgcgc cgggtgatgc gcggaggctc gtatctctgc 900
 catgattcct actgcaacag ataccgggtg gccgcccgc attcgaacac ccgggattcc 960
 acctcgggga ataccggttt ccgggtgcgtt ttcgatagtc cttga 1005

<210> 58
 <211> 334
 <212> PRT
 <213> *Corynebacterium efficiens*

<400> 58

Met Val Arg His Arg Leu Gly His Arg Pro Cys Thr Leu Arg Ile Thr
 1 5 10 15

Ser Met Ser Asn Cys Cys Ser Pro Ser Ser Ala Gln Trp Arg Thr Thr
 20 25 30

Thr Arg Asp Leu Ser Asp Pro Val Asn Pro Thr Thr Pro Cys Asn Pro
 35 40 45

Glu Gln Ser Arg Asp Ala Val Thr Leu Pro Gly Gly Ala Phe His Met
 50 55 60

Gly Asp His His Gly Glu Gly Tyr Pro Ala Asp Gly Glu Gly Pro Val
 65 70 75 80

His Glu Val His Leu Ala Pro Phe Gly Ile Asn Val Thr Thr Val Thr
 85 90 95

Asn Ala Glu Phe Gly Arg Phe Ile Glu Ala Thr Gly Tyr Thr Thr Thr
 100 105 110

Ala Glu Arg Tyr Gly Val Ser Ala Val Phe Tyr Ala Ala Phe Gln Gly
 115 120 125

Gln Arg Ala Asp Ile Leu Arg Gln Val Pro Gly Val Pro Trp Trp Leu
 130 135 140

Ala Val Lys Gly Ala Asn Trp Gln Arg Pro Asn Gly Pro Gly Ser Thr
 145 150 155 160

Leu Asp Gly Leu Glu Asp His Pro Val Val His Val Ser Trp Asp Asp
 165 170 175

Ala Val Ala Tyr Cys Thr Trp Ala Gly Gly Arg Leu Pro Thr Glu Ala
 180 185 190

Glu Trp Glu Tyr Ala Ala Arg Gly Gly Leu Gln Gly Ala Arg Tyr Ala
 195 200 205

Trp Gly Asp Asn Leu Ala Leu Asp Gly Arg Trp Asn Cys Asn Ile Trp
 210 215 220

Gln Gly Gly Phe Pro Met Glu Asn Thr Ala Ala Asp Gly Tyr Leu Thr
 225 230 235 240

Thr Ala Pro Val Lys Thr Tyr Thr Pro Asn Gly Tyr Gly Leu Trp Gln
 245 250 255

Met Ala Gly Asn Val Trp Glu Trp Cys Gln Asp Trp Phe Asp Ala Glu
 260 265 270

Tyr Tyr Ser Arg Ala Ser Ser Ile Asn Pro Arg Gly Pro Asp Thr Gly
 275 280 285

Ala Arg Arg Val Met Arg Gly Gly Ser Tyr Leu Cys His Asp Ser Tyr
 290 295 300

Cys Asn Arg Tyr Arg Val Ala Ala Arg Asn Ser Asn Thr Pro Asp Ser
 305 310 315 320

Thr Ser Gly Asn Thr Gly Phe Arg Cys Val Phe Asp Ser Pro
 325 330

<210> 59
 <211> 1017
 <212> DNA
 <213> Novosphingobium aromaticivorans

<400> 59
 atggcgcaac cattccgatac gacggcgggcc agtcgtacaa gtattgaacg ccatctcgaa 60
 cccaattgca ggagcacgtc gcgaatggtc gaacgccccg gcatgcgcct gatcgaaggc 120
 ggcactttca ccatgggctc ggaagccttc taccgaggagg aagcgccgct tcgccgggtg 180
 aaggtagaca gcttctggat cgatgaagcg ccggtgacga acgcacagtt cgccgcatte 240
 gtggaggcca cgggatacgt cactgtggcc gagatcgagc cggatcccaa ggactacccc 300
 ggcattgctcc cgggcatgga ccgcgcggga tcgctggtgt tccagaaaac agcaggggccg 360
 gtcgacatgg cggatgcgtc caactggtgg cactttacct ttggcgccctg ctggaagcat 420
 ccacttggac cgggcagttc catcgatggg atcgaggacc atcccgtcgt tcacgtcgcc 480
 tatgccgatg ccgaggccta tgccaaatgg gcgggcaagg atctgccgac cgaagccgag 540
 ttcgaatatg ctgcgcgcgg cgggttggac ggttcggaat tttcctgggg agacgaactc 600
 gcacctgaag gccggatgat ggccaactac tggcaaggcc tgtttccctt cgccaaccag 660
 tgccctgatg gctgggaacg gacatcgccc gtccgcaact tcccgcccaa cggctatggt 720
 ctttacgaca tgatcgggaa cacgtgggag tggacctgcg attggtgggc cgacaagccg 780
 ctgactccgc aaaggaaatc ggcattgctgc gcgatcagca atccgcgcgg cggcaagctc 840
 aaggacagct tcgaccctgc gcaaccgcga atgcgcatcg gccggaaggc cataaagggc 900
 ggttcgcacc tgtgtgcggc caattactgc cagcgtatc gccccgcagc acgccatcct 960

gaaatggttg ataccgcgac gacgcacatc ggcttcaggt gtgtggtgcg gccctga 1017

<210> 60
 <211> 338
 <212> PRT
 <213> Novosphingobium aromaticivorans

<400> 60

Met Ala Gln Pro Phe Arg Ser Thr Ala Ala Ser Arg Thr Ser Ile Glu
 1 5 10 15

Arg His Leu Glu Pro Asn Cys Arg Ser Thr Ser Arg Met Val Glu Arg
 20 25 30

Pro Gly Met Arg Leu Ile Glu Gly Gly Thr Phe Thr Met Gly Ser Glu
 35 40 45

Ala Phe Tyr Pro Glu Glu Ala Pro Leu Arg Arg Val Lys Val Asp Ser
 50 55 60

Phe Trp Ile Asp Glu Ala Pro Val Thr Asn Ala Gln Phe Ala Ala Phe
 65 70 75 80

Val Glu Ala Thr Gly Tyr Val Thr Val Ala Glu Ile Glu Pro Asp Pro
 85 90 95

Lys Asp Tyr Pro Gly Met Leu Pro Gly Met Asp Arg Ala Gly Ser Leu
 100 105 110

Val Phe Gln Lys Thr Ala Gly Pro Val Asp Met Ala Asp Ala Ser Asn
 115 120 125

Trp Trp His Phe Thr Phe Gly Ala Cys Trp Lys His Pro Leu Gly Pro
 130 135 140

Gly Ser Ser Ile Asp Gly Ile Glu Asp His Pro Val Val His Val Ala
 145 150 155 160

Tyr Ala Asp Ala Glu Ala Tyr Ala Lys Trp Ala Gly Lys Asp Leu Pro
 165 170 175

Thr Glu Ala Glu Phe Glu Tyr Ala Ala Arg Gly Gly Leu Asp Gly Ser
 180 185 190

Glu Phe Ser Trp Gly Asp Glu Leu Ala Pro Glu Gly Arg Met Met Ala
 195 200 205

Asn Tyr Trp Gln Gly Leu Phe Pro Phe Ala Asn Gln Cys Leu Asp Gly
 210 215 220

Trp Glu Arg Thr Ser Pro Val Arg Asn Phe Pro Pro Asn Gly Tyr Gly
 225 230 235 240

Leu Tyr Asp Met Ile Gly Asn Thr Trp Glu Trp Thr Cys Asp Trp Trp
 245 250 255

Ala Asp Lys Pro Leu Thr Pro Gln Arg Lys Ser Ala Cys Cys Ala Ile
 260 265 270

Ser Asn Pro Arg Gly Gly Lys Leu Lys Asp Ser Phe Asp Pro Ser Gln
 275 280 285

Pro Ala Met Arg Ile Gly Arg Lys Val Ile Lys Gly Gly Ser His Leu
 290 295 300

Cys Ala Ala Asn Tyr Cys Gln Arg Tyr Arg Pro Ala Ala Arg His Pro
 305 310 315 320

Glu Met Val Asp Thr Ala Thr Thr His Ile Gly Phe Arg Cys Val Val
 325 330 335

Arg Pro

<210> 61
 <211> 1119
 <212> DNA
 <213> Mesorhizobium loti

<400> 61
 atgggccac gaggtcgagg tcaaaaaccg catgaaaggc gacgcggtca tgttcgacat 60
 tgccgggaag ttctagccga tagcgggtgg gcggtgatg gagatgagca cgccgtgtca 120
 tttcgggatc tttcgatgaa cgcccctgcc gaagtcttcg agcgcgctgc agccgaacgg 180
 tcgtacccccg gaatggtctg gatccccggc ggtaccttcc tgatgggctc agacaaccac 240
 tatccggagg aggcaccggc ccaccgggctc agggctcgacg gcttctggat ggacaaattc 300

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accgtctcca accgcgactt cgaacgcttc gttgcggcga caggacatgt cactcttgcc 360
gagaaacccg ccaatcccga cgactatccc ggtgccttac ccgatctgct ggctccgtcc 420
tcgatgatgt tcaggaagcc ggccggccct gtcgaccttg gcaatcacta caattggtgg 480
gtctatgtcc gcggcgccaa ctggcgccat ccacgcgggc cggcaagtac aatcaagaag 540
gttgacagatc atccggtcgt gcatgtggcc tacgaggatg tcgtggccta tgccaactgg 600
gcaggcaagg aacttcccac cgaggccgag tgggaattcg cggcgcgagg cggcctcgat 660
gccgccgaat acgtctgggg caacgagctt acgccggccg ggaagcacat ggccaacatc 720
tggcaaggag actttcccta ccggaatact gtcgacgacg gttacgaata tacggcccca 780
gtaggctcgt tcccggccaa cgactacggt ctctacgaca tggccggcaa tgtctggcaa 840
tggacgaccg actggtacca ggaccacaag gcgatcgaca gcccgtgctg caccgctgtc 900
aatccgctg gcggccatcg cgaagcgagc tatgacaccc ggctacctga cgttaagatc 960
cctcgcaagg tcaccaaggg tggctcccat ctgtgcgcgc cgaactactg tcggcgctac 1020
cggcccgcgg cgcaatggc gcaaccgctc gacactgcaa tctcccatct cggctttcgc 1080
tgcacgtgc gaaggaaaat ggaattgaac gcgcagtaa 1119

```

<210> 62

<211> 372

<212> PRT

<213> Mesorhizobium loti

<400> 62

```

Met Gly Pro Arg Gly Arg Gly Gln Lys Pro His Glu Arg Arg Arg Gly
1           5           10          15

```

```

His Val Arg His Cys Arg Glu Val Leu Ala Asp Ser Gly Trp Ala Ala
          20          25          30

```

```

Asp Gly Asp Glu His Ala Val Ser Phe Arg Asp Leu Ser Met Asn Ala
          35          40          45

```

```

Pro Ala Glu Val Phe Glu Arg Ala Ala Ala Glu Arg Ser Tyr Pro Gly
          50          55          60

```

```

Met Val Trp Ile Pro Gly Gly Thr Phe Leu Met Gly Ser Asp Asn His
65          70          75          80

```

Tyr Pro Glu Glu Ala Pro Ala His Arg Val Arg Val Asp Gly Phe Trp
 85 90 95

Met Asp Lys Phe Thr Val Ser Asn Arg Asp Phe Glu Arg Phe Val Ala
 100 105 110

Ala Thr Gly His Val Thr Leu Ala Glu Lys Pro Ala Asn Pro Asp Asp
 115 120 125

Tyr Pro Gly Ala Leu Pro Asp Leu Leu Ala Pro Ser Ser Met Met Phe
 130 135 140

Arg Lys Pro Ala Gly Pro Val Asp Leu Gly Asn His Tyr Asn Trp Trp
 145 150 155 160

Val Tyr Val Arg Gly Ala Asn Trp Arg His Pro Arg Gly Pro Ala Ser
 165 170 175

Thr Ile Lys Lys Val Ala Asp His Pro Val Val His Val Ala Tyr Glu
 180 185 190

Asp Val Val Ala Tyr Ala Asn Trp Ala Gly Lys Glu Leu Pro Thr Glu
 195 200 205

Ala Glu Trp Glu Phe Ala Ala Arg Gly Gly Leu Asp Ala Ala Glu Tyr
 210 215 220

Val Trp Gly Asn Glu Leu Thr Pro Ala Gly Lys His Met Ala Asn Ile
 225 230 235 240

Trp Gln Gly Asp Phe Pro Tyr Arg Asn Thr Val Asp Asp Gly Tyr Glu
 245 250 255

Tyr Thr Ala Pro Val Gly Ser Phe Pro Ala Asn Asp Tyr Gly Leu Tyr
 260 265 270

Asp Met Ala Gly Asn Val Trp Gln Trp Thr Thr Asp Trp Tyr Gln Asp
 275 280 285

His Lys Ala Ile Asp Ser Pro Cys Cys Thr Ala Val Asn Pro Arg Gly
 290 295 300

Gly His Arg Glu Ala Ser Tyr Asp Thr Arg Leu Pro Asp Val Lys Ile

305 310 315 320
 Pro Arg Lys Val Thr Lys Gly Gly Ser His Leu Cys Ala Pro Asn Tyr
 325 330 335
 Cys Arg Arg Tyr Arg Pro Ala Ala Arg Met Ala Gln Pro Val Asp Thr
 340 345 350
 Ala Ile Ser His Leu Gly Phe Arg Cys Ile Val Arg Arg Lys Met Glu
 355 360 365
 Leu Asn Ala Gln
 370

<210> 63
 <211> 1251
 <212> DNA
 <213> Burkholderia fungorum

<400> 63
 atgaagagtg aaagagatcg agagcccgca aagtcgtccc gctcgaacgg gtcgggtcgca 60
 gcaacccaaa cgcgcgccgg tcgctgctgc aaactaatgt tgtggggcgc cctgctcgtc 120
 atactgcccc cctgtgtcgg cgccgcggtc agttgggcct tcacgccgca cgcacccgct 180
 caccgcgaaa tcgttttcgg cgacggcacg catggtccgc tcggcatggc gtgggtgccc 240
 ggcgggccagt tcctcatggg cagcgacgcc aaacaggcgc aaccgaacga acgccccgcg 300
 cacaaggtca aggtgcacgg cttctggatg gaccgccatc acgtgaccaa cgccgaattc 360
 cgccgcttcg tcgaagcgac cggctacgtc accacggccg agaagaaacc cgactgggag 420
 accctgaaag tccagttgcc gcccggcacg ccgcgcccgc ccgagagcgc gatggtggcg 480
 ggtgcaatgg tgttcgtcgg caccagccgt cccgtgccgc tagacgacta ttcgcagtgg 540
 tggcgctatg tgcctggcgc taactggcgt catccagccg ggctgagag caacatcatc 600
 ggtaaagatg atcaccccggt ggttcaagtg tcctacgaag atgcgcaggc ttatgcgaaa 660
 tgggcccggca agcgtctgcc gaccgaagcc gaatgggaat tcgccgcgcg cggcgggctc 720
 gaacaggcca cgtatgcgtg gggcgatcag ttctctccca acggcaaaca gatggccaac 780
 gtctggcagg gccagcagcc gcagtcttcc cccgttgtca acccgaaagc ggggtggcgcg 840
 ctcggtacaa gtccggtggg tactttcccg gccaacggct acggccttcc cgacatgacc 900
 ggcaacgcct ggcagtgggt tgccgactgg tatcgcgcgg atcagttcag gcgtgaggcg 960

gtaagcacca ggcgcatcga caatccggtg ggcccagagcg agtcgtggga ccccgagac 1020
 cagggcggtgc ccgtcaacgc gcccaagcgt gtcacacgcg gcggttcggt cctctgcaac 1080
 gaaatctatt gcctgagcta ccggcccagc gcgagacgcg gcaccgatcc ctacaacagc 1140
 atgtcgcatc tgggcttccg gctgggtgatg gacgaagaca cctggaaaga agccggtgct 1200
 cgccaggctt cggcgaaagc tgccggcgcg cctggaaccc ctggcggcta g 1251

<210> 64
 <211> 416
 <212> PRT
 <213> Burkholderia fungorum

<400> 64

Met Lys Ser Glu Arg Asp Arg Glu Pro Ala Lys Ser Ser Arg Ser Asn
 1 5 10 15

Gly Ser Val Ala Ala Thr Gln Thr Arg Ala Gly Arg Val Arg Lys Leu
 20 25 30

Met Leu Trp Gly Ala Leu Leu Val Ile Leu Pro Ala Cys Val Gly Ala
 35 40 45

Ala Val Ser Trp Ala Phe Thr Pro His Ala Pro Ala His Pro Gln Ile
 50 55 60

Val Phe Gly Asp Gly Thr His Gly Pro Leu Gly Met Ala Trp Val Pro
 65 70 75 80

Gly Gly Gln Phe Leu Met Gly Ser Asp Ala Lys Gln Ala Gln Pro Asn
 85 90 95

Glu Arg Pro Ala His Lys Val Lys Val His Gly Phe Trp Met Asp Arg
 100 105 110

His His Val Thr Asn Ala Glu Phe Arg Arg Phe Val Glu Ala Thr Gly
 115 120 125

Tyr Val Thr Thr Ala Glu Lys Lys Pro Asp Trp Glu Thr Leu Lys Val
 130 135 140

Gln Leu Pro Pro Gly Thr Pro Arg Pro Pro Glu Ser Ala Met Val Ala
 145 150 155 160

Gly Ala Met Val Phe Val Gly Thr Ser Arg Pro Val Pro Leu Asp Asp
 165 170 175

Tyr Ser Gln Trp Trp Arg Tyr Val Pro Gly Ala Asn Trp Arg His Pro
 180 185 190

Ala Gly Pro Glu Ser Asn Ile Ile Gly Lys Asp Asp His Pro Val Val
 195 200 205

Gln Val Ser Tyr Glu Asp Ala Gln Ala Tyr Ala Lys Trp Ala Gly Lys
 210 215 220

Arg Leu Pro Thr Glu Ala Glu Trp Glu Phe Ala Ala Arg Gly Gly Leu
 225 230 235 240

Glu Gln Ala Thr Tyr Ala Trp Gly Asp Gln Phe Ser Pro Asn Gly Lys
 245 250 255

Gln Met Ala Asn Val Trp Gln Gly Gln Gln Pro Gln Ser Phe Pro Val
 260 265 270

Val Asn Pro Lys Ala Gly Gly Ala Leu Gly Thr Ser Pro Val Gly Thr
 275 280 285

Phe Pro Ala Asn Gly Tyr Gly Leu Ser Asp Met Thr Gly Asn Ala Trp
 290 295 300

Gln Trp Val Ala Asp Trp Tyr Arg Ala Asp Gln Phe Arg Arg Glu Ala
 305 310 315 320

Val Ser Thr Ser Ala Ile Asp Asn Pro Val Gly Pro Ser Glu Ser Trp
 325 330 335

Asp Pro Ala Asp Gln Gly Val Pro Val Asn Ala Pro Lys Arg Val Thr
 340 345 350

Arg Gly Gly Ser Phe Leu Cys Asn Glu Ile Tyr Cys Leu Ser Tyr Arg
 355 360 365

Pro Ser Ala Arg Arg Gly Thr Asp Pro Tyr Asn Ser Met Ser His Leu
 370 375 380

Gly Phe Arg Leu Val Met Asp Glu Asp Thr Trp Lys Glu Ala Gly Ala
 385 390 395 400

Arg Gln Ala Ser Ala Lys Ala Ala Gly Ala Pro Gly Thr Pro Gly Gly
 405 410 415

<210> 65
 <211> 912
 <212> DNA
 <213> *Sinorhizobium meliloti*

<400> 65
 atggtctggg ttcccggagc gaccttcacg atgggggtcga acgaccatta cccggaggaa 60
 gcgcccgtgc atccggtaac cgtcgacgga ttctggatcg atgtgacacc ggtaacgaac 120
 cgccagtttc tcgaattcgt aaatgacgac gggcatgtga ccttcgacga aagaaagccg 180
 cgcgccgaag actatccggg cgctccgcca tccaatctaa gggccgggtc gctcgtcttc 240
 acacccccga agcagaccgt gcaggggaac gatataatcg agtgggtgat attcacgctg 300
 ggtgccaact ggcggcaccc gctcggggcg aagagcagca tcggagcgat tctggatcat 360
 ccggtcgtcc atgtcgctta cagcgacgca aaggcctatg ccgaatgggc cggcaaggac 420
 ctcccgaccg agaccgagtg ggagctggcg gcccgcggcg gcctcgatgg ggctgaattt 480
 tcctggggcg gcgagcttgc gccgggcgga aatcacatgg ccaataactg gcaggggaagt 540
 tttccggtcg agaattctat ggacgatggt ttccgacgaa catcgccggt cagattttac 600
 ccgccaacg gctacggcct ctacgacatg atcggaatg tgtgggagtg gaccacggat 660
 tactggtccg tgcgccaccc ggaagcggcc gccaaagcctt gctgcattcc gagcaatccc 720
 cgcaatgccg atgccgatgc gagtatcgat ccggcggcga gcgtgaaagt tccgcgcccg 780
 gtgctcaagg gtggatcgca tctctgcgcg ccgaactact gccggcggtg ccgccctgcg 840
 gcgaggcacg cccaggaaat cgacacgacg accagccatg tcggtttccg atgtgtcagg 900
 cgcggttcgat aa 912

<210> 66
 <211> 303
 <212> PRT
 <213> *Sinorhizobium meliloti*

<400> 66

Met Val Trp Val Pro Gly Ala Thr Phe Met Met Gly Ser Asn Asp His
 1 5 10 15

Tyr Pro Glu Glu Ala Pro Val His Pro Val Thr Val Asp Gly Phe Trp
 20 25 30

Ile Asp Val Thr Pro Val Thr Asn Arg Gln Phe Leu Glu Phe Val Asn
 35 40 45

Ala Thr Gly His Val Thr Phe Ala Glu Arg Lys Pro Arg Ala Glu Asp
 50 55 60

Tyr Pro Gly Ala Pro Pro Ser Asn Leu Arg Ala Gly Ser Leu Val Phe
 65 70 75 80

Thr Pro Pro Lys Arg Pro Leu Gln Gly Thr Asp Ile Ser Gln Trp Trp
 85 90 95

Ile Phe Thr Leu Gly Ala Asn Trp Arg His Pro Leu Gly Arg Lys Ser
 100 105 110

Ser Ile Gly Ala Ile Leu Asp His Pro Val Val His Val Ala Tyr Ser
 115 120 125

Asp Ala Lys Ala Tyr Ala Glu Trp Ala Gly Lys Asp Leu Pro Thr Glu
 130 135 140

Thr Glu Trp Glu Leu Ala Ala Arg Gly Gly Leu Asp Gly Ala Glu Phe
 145 150 155 160

Ser Trp Gly Gly Glu Leu Ala Pro Gly Gly Asn His Met Ala Asn Thr
 165 170 175

Trp Gln Gly Ser Phe Pro Val Glu Asn Ser Met Asp Asp Gly Phe Ala
 180 185 190

Arg Thr Ser Pro Val Arg Phe Tyr Pro Pro Asn Gly Tyr Gly Leu Tyr
 195 200 205

Asp Met Ile Gly Asn Val Trp Glu Trp Thr Thr Asp Tyr Trp Ser Val
 210 215 220

Arg His Pro Glu Ala Ala Ala Lys Pro Cys Cys Ile Pro Ser Asn Pro
 225 230 235 240

Arg Asn Ala Asp Ala Asp Ala Ser Ile Asp Pro Ala Ala Ser Val Lys
 245 250 255

Val Pro Arg Arg Val Leu Lys Gly Gly Ser His Leu Cys Ala Pro Asn
 260 265 270

Tyr Cys Arg Arg Tyr Arg Pro Ala Ala Arg His Ala Gln Glu Ile Asp
 275 280 285

Thr Thr Thr Ser His Val Gly Phe Arg Cys Val Arg Arg Val Arg
 290 295 300

<210> 67
 <211> 1065
 <212> DNA
 <213> Microscilla sp.

<400> 67
 atgaaataca ttttttttagt tcttttctta tgggccttga cccgatgtac cggaaagtat 60
 gaggacaaga gagtggaaac tgatacttcc agacaaaaag ccgaagcgtc agatataaaa 120
 gttcccgaag gaatggctta tattcccgcg ggccagtaca tgatgggagg taaatcagac 180
 caggcttata aggatgaata tccccgccat aacgtgaagg ttccggcttt ttatatggac 240
 cttacagaag tgaccaatgc ggagtttaag cggtttgtag acgaaacggg ctacgtgacc 300
 attgctgaga aagatattga ctgggaagag ttaaagtctc aggtgccaca gggtagcccg 360
 aagcctcctg attctgtgct tcaggcaggt tcaactggttt tcaagcagac agatgaaccc 420
 gtttctctcc aggattattc acagtgggtg gaatggacta tcggagccaa ctggcgaaat 480
 ccggaggggtc caggtagtac gattgaggat cgtatggatc atccgggtgg acacgtttcc 540
 tttgaagatg tccaagcgtg tgcggattgg gccggtaagc gcctgcctac tgaggcagaa 600
 tgggaatggg ccgccatggg aggccaaaat gacgtgaaat atccatgggg aaatgaatcg 660
 gtogaacaag catccgataa agcaaaacttt tggcagggga attttccaca tcaaaactat 720
 gccctcgatg gattcgaacg caccgcccct gtacgctcct tcccagcgaa tgggtacggc 780
 ctatatgata tggctggcaa tgtgtgggaa tgggtgccagg ataagtatga tgtcaatgct 840
 tatgaaagct ataagcaaaa aggactgaca gaagacccca cgggttctga gcactacaac 900
 gaccctaggg aaccgtatac tctaagcat gtgatcagag ggggttcttt cctatgcaat 960
 gacagctact gtagtgggta tcgtgtttca cgtcgtatga gttccagtag agattcaggt 1020
 tttaatcata cgggattcag gtgtgtgaaa gatgtaaatt gatag 1065

<210> 68
 <211> 354
 <212> PRT
 <213> Microscilla sp.

<400> 68

Met Lys Tyr Ile Phe Leu Val Leu Phe Leu Trp Ala Leu Thr Arg Cys
 1 5 10 15

Thr Gly Lys Tyr Glu Asp Lys Arg Val Glu Thr Asp Thr Ser Arg Pro
 20 25 30

Lys Ala Glu Ala Ser Asp Ile Lys Val Pro Glu Gly Met Ala Tyr Ile
 35 40 45

Pro Ala Gly Gln Tyr Met Met Gly Gly Lys Ser Asp Gln Ala Tyr Lys
 50 55 60

Asp Glu Tyr Pro Arg His Asn Val Lys Val Ser Ala Phe Tyr Met Asp
 65 70 75 80

Leu Thr Glu Val Thr Asn Ala Glu Phe Lys Arg Phe Val Asp Glu Thr
 85 90 95

Gly Tyr Val Thr Ile Ala Glu Lys Asp Ile Asp Trp Glu Glu Leu Lys
 100 105 110

Ser Gln Val Pro Gln Gly Thr Pro Lys Pro Pro Asp Ser Val Leu Gln
 115 120 125

Ala Gly Ser Leu Val Phe Lys Gln Thr Asp Glu Pro Val Ser Leu Gln
 130 135 140

Asp Tyr Ser Gln Trp Trp Glu Trp Thr Ile Gly Ala Asn Trp Arg Asn
 145 150 155 160

Pro Glu Gly Pro Gly Ser Thr Ile Glu Asp Arg Met Asp His Pro Val
 165 170 175

Val His Val Ser Phe Glu Asp Val Gln Ala Tyr Ala Asp Trp Ala Gly
 180 185 190

Lys Arg Leu Pro Thr Glu Ala Glu Trp Glu Trp Ala Ala Met Gly Gly
 195 200 205

Gln Asn Asp Val Lys Tyr Pro Trp Gly Asn Glu Ser Val Glu Gln Ala
 210 215 220

Ser Asp Lys Ala Asn Phe Trp Gln Gly Asn Phe Pro His Gln Asn Tyr
 225 230 235 240

Ala Leu Asp Gly Phe Glu Arg Thr Ala Pro Val Arg Ser Phe Pro Ala
 245 250 255

Asn Gly Tyr Gly Leu Tyr Asp Met Ala Gly Asn Val Trp Glu Trp Cys
 260 265 270

Gln Asp Lys Tyr Asp Val Asn Ala Tyr Glu Ser Tyr Lys Gln Lys Gly
 275 280 285

Leu Thr Glu Asp Pro Thr Gly Ser Glu His Tyr Asn Asp Pro Arg Glu
 290 295 300

Pro Tyr Thr Pro Lys His Val Ile Arg Gly Gly Ser Phe Leu Cys Asn
 305 310 315 320

Asp Ser Tyr Cys Ser Gly Tyr Arg Val Ser Arg Arg Met Ser Ser Ser
 325 330 335

Arg Asp Ser Gly Phe Asn His Thr Gly Phe Arg Cys Val Lys Asp Val
 340 345 350

Asn Gly

<210> 69

<211> 876

<212> DNA

<213> Pseudomonas putida KT2440

<400> 69

atggtgcacg tgccggggcgg cgagttcagc tttggttcaa gccgctttta cgacgaagaa 60

ggccccgctc accccgccaa ggtgtccggc ttctggattg acgtgcatcc ggtcaccaac 120

gccagttcg cgcgcttcgt caaggccacg gggatatgtca cccatgccga gcgcggtacc 180

cgtgtcgagg acgaccctgc cctgcccagc gcgctgcgga taccgggtgc gatggtgttt 240


```

catcaggggtg cggacgtgct cggccccggc tggcagttcg tgcccggcgc caactggcga      300
caccgcgaag ggccgggcag cagcctggcc gggctggaca accatccggt ggtgcagatc      360
gccctggaag atgcccaggc ctatgcccgc tgggcaggcc gcgaactgcc cagcgaggcg      420
cagctggaat acgccatgcg cggcggcctg accgatgccg acttcagctg gggtagacc      480
gagcagccca agggcaagct catggccaat acctggcagg gtcagttccc ttatcgcaat      540
gcggcgaagg atggttttac cggtagatcg cccgtgggtt gcttcccggc caacggcttt      600
ggcctgttcg atgccggcgg caatgtctgg gagctgactc gcacgggcta tcggccaggc      660
catgacgcac agcgcgacgc caagctcgac ccctcaggcc cggccctgag tgacagcttc      720
gacccggcag accccggcgt gccgggtggcg gtaatcaaag gcggctcgca cctgtgttcg      780
gcggaccgct gcatgcgcta ccgcccctcg gcacgccagc cgcagccggt gttcatgacg      840
acctcgcacg tgggtttcag aacgattcgg caatga                                  876

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```

<210> 70
<211> 291
<212> PRT
<213> Pseudomonas putida KT2440

```

```

<400> 70

```

```

Met Val His Val Pro Gly Gly Glu Phe Ser Phe Gly Ser Ser Arg Phe
1           5           10           15

```

```

Tyr Asp Glu Glu Gly Pro Pro His Pro Ala Lys Val Ser Gly Phe Trp
          20           25           30

```

```

Ile Asp Val His Pro Val Thr Asn Ala Gln Phe Ala Arg Phe Val Lys
          35           40           45

```

```

Ala Thr Gly Tyr Val Thr His Ala Glu Arg Gly Thr Arg Val Glu Asp
          50           55           60

```

```

Asp Pro Ala Leu Pro Asp Ala Leu Arg Ile Pro Gly Ala Met Val Phe
65           70           75           80

```

```

His Gln Gly Ala Asp Val Leu Gly Pro Gly Trp Gln Phe Val Pro Gly
          85           90           95

```

```

Ala Asn Trp Arg His Pro Gln Gly Pro Gly Ser Ser Leu Ala Gly Leu
          100          105          110

```

Asp Asn His Pro Val Val Gln Ile Ala Leu Glu Asp Ala Gln Ala Tyr
 115 120 125

Ala Arg Trp Ala Gly Arg Glu Leu Pro Ser Glu Ala Gln Leu Glu Tyr
 130 135 140

Ala Met Arg Gly Gly Leu Thr Asp Ala Asp Phe Ser Trp Gly Thr Thr
 145 150 155 160

Glu Gln Pro Lys Gly Lys Leu Met Ala Asn Thr Trp Gln Gly Gln Phe
 165 170 175

Pro Tyr Arg Asn Ala Ala Lys Asp Gly Phe Thr Gly Thr Ser Pro Val
 180 185 190

Gly Cys Phe Pro Ala Asn Gly Phe Gly Leu Phe Asp Ala Gly Gly Asn
 195 200 205

Val Trp Glu Leu Thr Arg Thr Gly Tyr Arg Pro Gly His Asp Ala Gln
 210 215 220

Arg Asp Ala Lys Leu Asp Pro Ser Gly Pro Ala Leu Ser Asp Ser Phe
 225 230 235 240

Asp Pro Ala Asp Pro Gly Val Pro Val Ala Val Ile Lys Gly Gly Ser
 245 250 255

His Leu Cys Ser Ala Asp Arg Cys Met Arg Tyr Arg Pro Ser Ala Arg
 260 265 270

Gln Pro Gln Pro Val Phe Met Thr Thr Ser His Val Gly Phe Arg Thr
 275 280 285

Ile Arg Gln
 290

<210> 71
 <211> 780
 <212> DNA
 <213> Ralstonia metallidurans

<400> 71
 atgggtcgcg gcgggatggt gttcgtcggc accaacagcc cggtgccgct gcgcgaatac

```

tggcgctgggt ggcgcttcgt acctggcgcg gactggcgctc acccgaccgg cccggggcagt 120
tccatcgaag gcaaggacaa tcattcccgtc gtgcaggtct cgtatgaaga cgcgcaggcg 180
tacgccaagt gggccggcaa gcgtctgccc accgaggccg agtgggagtt tgccgcccg 240
ggcgccctgg agcaggccac ctacgcctgg ggtgacaagt tcgcgccgga tggccggcag 300
atggcgaatg tctggcaggg ccagcaggtg cagccgttcc cggtggtcag cgccaaggcg 360
ggcgcgcgcg ctggcaccag tgctgtcggc acgttcccgg gcaatggcta tgggctctat 420
gacatgaccg gcaacgcctg gcagtgggtg gccgactggt atcgcgcgga ccagttccgc 480
cgcgaagcca cgggtggcggc agtgctgcag aatccgaccg gcccggccga ttcgtgggac 540
ccgaccgaac ctggcggtgcc ggtgtcggcg cccaagcggg tcacgcgcgg tggctcgttc 600
ctctgcaacg aggacttctg cctcagctac cgcccgagt cccggcgcgg taccgaccg 660
tacaccagca tgtcgcacct aggcttccgg ctctgatgg atgacgccg ttgggcagaa 720
gttcgcaagc agccagccgt ggcaatggcc gcgggcgggc agcagaacgt gcagaaataa 780

```

```

<210> 72
<211> 259
<212> PRT
<213> Ralstonia metallidurans

```

```
<400> 72
```

```

Met Val Ala Gly Gly Met Val Phe Val Gly Thr Asn Ser Pro Val Pro
1           5           10           15

Leu Arg Glu Tyr Trp Arg Trp Trp Arg Phe Val Pro Gly Ala Asp Trp
          20           25           30

Arg His Pro Thr Gly Pro Gly Ser Ser Ile Glu Gly Lys Asp Asn His
          35           40           45

Pro Val Val Gln Val Ser Tyr Glu Asp Ala Gln Ala Tyr Ala Lys Trp
          50           55           60

Ala Gly Lys Arg Leu Pro Thr Glu Ala Glu Trp Glu Phe Ala Ala Arg
65           70           75           80

Gly Gly Leu Glu Gln Ala Thr Tyr Ala Trp Gly Asp Lys Phe Ala Pro
          85           90           95

```

Asp Gly Arg Gln Met Ala Asn Val Trp Gln Gly Gln Gln Val Gln Pro
 100 105 110

Phe Pro Val Val Ser Ala Lys Ala Gly Gly Ala Ala Gly Thr Ser Ala
 115 120 125

Val Gly Thr Phe Pro Gly Asn Gly Tyr Gly Leu Tyr Asp Met Thr Gly
 130 135 140

Asn Ala Trp Gln Trp Val Ala Asp Trp Tyr Arg Ala Asp Gln Phe Arg
 145 150 155 160

Arg Glu Ala Thr Val Ala Ala Val Leu Gln Asn Pro Thr Gly Pro Ala
 165 170 175

Asp Ser Trp Asp Pro Thr Glu Pro Gly Val Pro Val Ser Ala Pro Lys
 180 185 190

Arg Val Thr Arg Gly Gly Ser Phe Leu Cys Asn Glu Asp Phe Cys Leu
 195 200 205

Ser Tyr Arg Pro Ser Ala Arg Arg Gly Thr Asp Pro Tyr Thr Ser Met
 210 215 220

Ser His Leu Gly Phe Arg Leu Val Met Asp Asp Ala Arg Trp Ala Glu
 225 230 235 240

Val Arg Lys Gln Pro Ala Val Ala Met Ala Ala Gly Gly Gln Gln Asn
 245 250 255

Val Gln Lys

<210> 73

<211> 876

<212> DNA

<213> Prochlorococcus marinus

<400> 73

gtgaccacat ctttgccagt agagatggta accatccccg cagggctcta tcgagttggc 60

tgtgatcgct gctatccgga tggttcagtt cgctgctatc cggaggaaac acccgcgcca 120

gaagtgcagc ttgactcatt ccagatcgac gtagggccag tcaccaatgc ccagttccga 180

gctttcggtta gcgccacgca gcatctcaca gtctcggagc taccaccta tccaacgctc 240

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tatcccgatc tagcgccga ggaacgcac cctgaatcag ttgtctttca accgcctcca 300
gcaacggtgg atcgacgcaa acccttgagc tggtaggacc tcatggctgg ggctgattgg 360
cgatcatccc aaggacccga aagcacgac gatggccttg atgatcacc tgctgtgcat 420
gtcgcttatg ccgacgccat cgcctatgcc cattgggctg gcaagcgtct cccctctgct 480
gaagagtggg aagtagccgc ccgcggggggt cttgtcgatg cccaatacgc ctgggggaat 540
gaactcactc ccaataaccg ctggatggcg aacatctggc aaggtccttt cccttggcac 600
aacgaggagc tagacggctg gttctggacc tcgcccgttg gcagctttcc tgccaacggc 660
tatggactct tggatgtttg cggcaatgtg tgggaatgga ccaactctgt ttatcccgctg 720
gcgtcaggcc accaggaacg gcgaactatc aaaggcggat cgtttctctg cgcagataat 780
tactgcgtac gttatcgacc ctctgcacta caaggccaga cagtagacac tgccacctgt 840
cacatgggct ttcgctgtgc aaaaggaggg ccttga 876

```

```

<210> 74
<211> 291
<212> PRT
<213> Prochlorococcus marinus

```

```
<400> 74
```

```

Met Thr Thr Ser Leu Pro Val Glu Met Val Thr Ile Pro Ala Gly Leu
1           5           10           15

```

```

Tyr Arg Val Gly Cys Asp Arg Cys Tyr Pro Asp Gly Ser Val Arg Cys
20           25           30

```

```

Tyr Pro Glu Glu Thr Pro Ala Arg Glu Val Gln Leu Asp Ser Phe Gln
35           40           45

```

```

Ile Asp Val Gly Pro Val Thr Asn Ala Gln Phe Arg Ala Phe Val Ser
50           55           60

```

```

Ala Thr Gln His Leu Thr Val Ser Glu Leu Pro Pro Asp Pro Thr Leu
65           70           75           80

```

```

Tyr Pro Asp Leu Ala Pro Glu Glu Arg Ile Pro Glu Ser Val Val Phe
85           90           95

```

```

Gln Pro Pro Pro Ala Thr Val Asp Arg Ser Lys Pro Leu Ser Trp Trp
100           105           110

```

Thr Leu Met Ala Gly Ala Asp Trp Arg His Pro Gln Gly Pro Glu Ser
 115 120 125

Thr Ile Asp Gly Leu Asp Asp His Pro Val Val His Val Ala Tyr Ala
 130 135 140

Asp Ala Ile Ala Tyr Ala His Trp Ala Gly Lys Arg Leu Pro Ser Ala
 145 150 155 160

Glu Glu Trp Glu Val Ala Ala Arg Gly Gly Leu Val Asp Ala Gln Tyr
 165 170 175

Ala Trp Gly Asn Glu Leu Thr Pro Asn Asn Arg Trp Met Ala Asn Ile
 180 185 190

Trp Gln Gly Pro Phe Pro Trp His Asn Glu Glu Leu Asp Gly Trp Phe
 195 200 205

Trp Thr Ser Pro Val Gly Ser Phe Pro Ala Asn Gly Tyr Gly Leu Leu
 210 215 220

Asp Val Cys Gly Asn Val Trp Glu Trp Thr Asn Ser Val Tyr Pro Val
 225 230 235 240

Ala Ser Gly His Gln Glu Arg Arg Thr Ile Lys Gly Gly Ser Phe Leu
 245 250 255

Cys Ala Asp Asn Tyr Cys Val Arg Tyr Arg Pro Ser Ala Leu Gln Gly
 260 265 270

Gln Thr Val Asp Thr Ala Thr Cys His Met Gly Phe Arg Cys Ala Lys
 275 280 285

Gly Gly Pro
 290

<210> 75
 <211> 1017
 <212> DNA
 <213> Caulobacter crescentus CB15

<400> 75
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ccggcgccca aggcttgctt ggcggacctg ccggttccag atccccagaa ccgcacggcg 120
 ggtatggttc ggctggcggg cggcgacttc cagatgggcg ctgcgccgct gcgtccggag 180
 gagggaccgc cccagacggg cacgggtccc cgtttctgga tcgatcagac agaggtcacc 240
 aacgccgcct tcgcgcggtt cgtcgaggcc acgggttatc gcaccgtggc cgagcgaccg 300
 ctcgaccccg cgcgctacgc ccacgtaccg gcggcgcgag ggctccggc ctcgctcgtc 360
 ttcgtggggg cgaagggggc gaggtcggac gatccttccc aatggtggca ggtgatcccc 420
 ggcgccgact ggcggcatcc cgaaggtccc ggctcgaaca tccggggcag ggacgcctgg 480
 ccggtggtgc atatcgctg ggaggacgcc atggcctacg cccgctggct gggccgtgac 540
 ctgcccacag aggccgaatg ggagtacgcc gcgcgcggcg ggctggttgg caagcgctac 600
 acctggggcg accaggctca ggatcctgca aagccgcgcg ccaatacttg gcaaggcgty 660
 ttcccggccc aggaccttgg caatgacggc ttcaaggcca agcccgcgcc ggtcggctgc 720
 ttcccgccca acggctatgg cctgcgcgac atggccggca atgtctggga gtggaccgc 780
 gactggttca agccgggcct ggatccggtc agcgtcctcg aaaccggcg gccgcccag 840
 gcccgcgcg tggatcccga ggaccgaac acgccaagc acgtcgtgaa gggcggttcg 900
 ttctgtgcg ccgacgacta ctgcttcgc tatcgacctg cggcggaac gccggggccg 960
 ccggacagcg gcgcatcgca tgtcggttcc cgcaccgtgc tccgcgccga gcgctga 1017

<210> 76
 <211> 338
 <212> PRT
 <213> *Caulobacter crescentus* CB15

<400> 76

Met Gly Lys Leu Thr Ala Leu Pro Val Leu Met Leu Leu Ala Leu Ala
 1 5 10 15

Gly Cys Gly Gln Pro Ala Pro Lys Ala Cys Leu Ala Asp Leu Pro Val
 20 25 30

Pro Asp Pro Gln Asn Arg Thr Ala Gly Met Val Arg Leu Ala Gly Gly
 35 40 45

Asp Phe Gln Met Gly Ala Ala Pro Leu Arg Pro Glu Glu Gly Pro Pro
 50 55 60

Gln Thr Val Thr Val Pro Pro Phe Trp Ile Asp Gln Thr Glu Val Thr
65 70 75 80

Asn Ala Ala Phe Ala Arg Phe Val Glu Ala Thr Gly Tyr Arg Thr Val
85 90 95

Ala Glu Arg Pro Leu Asp Pro Ala Arg Tyr Ala His Val Pro Ala Ala
100 105 110

Gln Arg Arg Pro Ala Ser Leu Val Phe Val Gly Ala Lys Gly Ala Arg
115 120 125

Ser Asp Asp Pro Ser Gln Trp Trp Gln Val Ile Pro Gly Ala Asp Trp
130 135 140

Arg His Pro Glu Gly Pro Gly Ser Asn Ile Arg Gly Arg Asp Ala Trp
145 150 155 160

Pro Val Val His Ile Ala Trp Glu Asp Ala Met Ala Tyr Ala Arg Trp
165 170 175

Leu Gly Arg Asp Leu Pro Thr Glu Ala Glu Trp Glu Tyr Ala Ala Arg
180 185 190

Gly Gly Leu Val Gly Lys Arg Tyr Thr Trp Gly Asp Gln Ala Gln Asp
195 200 205

Pro Ala Lys Pro Arg Ala Asn Thr Trp Gln Gly Val Phe Pro Ala Gln
210 215 220

Asp Leu Gly Asn Asp Gly Phe Lys Ala Lys Pro Ala Pro Val Gly Cys
225 230 235 240

Phe Pro Pro Asn Gly Tyr Gly Leu Arg Asp Met Ala Gly Asn Val Trp
245 250 255

Glu Trp Thr Arg Asp Trp Phe Lys Pro Gly Leu Asp Pro Val Ser Val
260 265 270

Leu Glu Thr Gly Gly Pro Pro Glu Ala Arg Ala Leu Asp Pro Glu Asp
275 280 285

Pro Asn Thr Pro Lys His Val Val Lys Gly Gly Ser Phe Leu Cys Ala

290

295

300

Asp Asp Tyr Cys Phe Arg Tyr Arg Pro Ala Ala Arg Thr Pro Gly Pro
 305 310 315 320

Pro Asp Ser Gly Ala Ser His Val Gly Phe Arg Thr Val Leu Arg Ala
 325 330 335

Glu Arg

<210> 77

<211> 900

<212> DNA

<213> Mycobacterium tuberculosis H37Rv

<400> 77

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 taccgccgaag aagcgccgat tcataccgtg accgtgcgcg cctttgcggt agagcgacac 120
 ccggtgacca acgcgcaatt tgccgaattc gtctccgcga caggctatgt gacgggtgca 180
 gaacaacccc ttgaccccgg gctctacca ggagtggacg cagcagacct gtgtcccggg 240
 gcgatggtgt tttgtccgac ggccggggccg gtcgacctgc gtgactggcg gcaatgggtg 300
 gactgggtac ctggcgccctg ctggcgccat ccgtttggcc gggacagcga tatcgccgac 360
 cgagccggcc acccggtcgt acagggtggcc tatccggacg ccgtggccta cgcacgatgg 420
 gctggtcgac gcctaccgac cgaggccgag tgggagtacg cggcccgtgg cggaaccacg 480
 gcaacctatg cgtggggcga ccaggagaag ccggggggcga tgctcatggc gaacacctgg 540
 cagggccggt ttccttaccg caacgacggt gcattgggct gggtgggaaac ctccccggtg 600
 ggcaggtttc cggccaacgg gtttggcttg ctcgacatga tcggaaacgt ttgggagtgg 660
 accaccaccg agttctatcc acaccatcgc atcgatccac cctcgacggc ctgctgcgca 720
 ccggtcaagc tcgctacagc cgccgaccg acgatcagcc agaccctcaa gggcggtcgc 780
 cacctgtgcg cgccggagta ctgccaccgc taccgcccgg cggcgcgctc gccgcagtcg 840
 caggacaccg cgaccacca tatcgggttc cgggtgctgg ccgaccgggt gtccgggtag 900

<210> 78

<211> 299

<212> PRT

<213> Mycobacterium tuberculosis H37Rv

<400> 78

Met Leu Thr Glu Leu Val Asp Leu Pro Gly Gly Ser Phe Arg Met Gly
 1 5 10 15

Ser Thr Arg Phe Tyr Pro Glu Glu Ala Pro Ile His Thr Val Thr Val
 20 25 30

Arg Ala Phe Ala Val Glu Arg His Pro Val Thr Asn Ala Gln Phe Ala
 35 40 45

Glu Phe Val Ser Ala Thr Gly Tyr Val Thr Val Ala Glu Gln Pro Leu
 50 55 60

Asp Pro Gly Leu Tyr Pro Gly Val Asp Ala Ala Asp Leu Cys Pro Gly
 65 70 75 80

Ala Met Val Phe Cys Pro Thr Ala Gly Pro Val Asp Leu Arg Asp Trp
 85 90 95

Arg Gln Trp Trp Asp Trp Val Pro Gly Ala Cys Trp Arg His Pro Phe
 100 105 110

Gly Arg Asp Ser Asp Ile Ala Asp Arg Ala Gly His Pro Val Val Gln
 115 120 125

Val Ala Tyr Pro Asp Ala Val Ala Tyr Ala Arg Trp Ala Gly Arg Arg
 130 135 140

Leu Pro Thr Glu Ala Glu Trp Glu Tyr Ala Ala Arg Gly Gly Thr Thr
 145 150 155 160

Ala Thr Tyr Ala Trp Gly Asp Gln Glu Lys Pro Gly Gly Met Leu Met
 165 170 175

Ala Asn Thr Trp Gln Gly Arg Phe Pro Tyr Arg Asn Asp Gly Ala Leu
 180 185 190

Gly Trp Val Gly Thr Ser Pro Val Gly Arg Phe Pro Ala Asn Gly Phe
 195 200 205

Gly Leu Leu Asp Met Ile Gly Asn Val Trp Glu Trp Thr Thr Thr Glu
 210 215 220

Phe Tyr Pro His His Arg Ile Asp Pro Pro Ser Thr Ala Cys Cys Ala
 225 230 235 240

Pro Val Lys Leu Ala Thr Ala Ala Asp Pro Thr Ile Ser Gln Thr Leu
 245 250 255

Lys Gly Gly Ser His Leu Cys Ala Pro Glu Tyr Cys His Arg Tyr Arg
 260 265 270

Pro Ala Ala Arg Ser Pro Gln Ser Gln Asp Thr Ala Thr Thr His Ile
 275 280 285

Gly Phe Arg Cys Val Ala Asp Pro Val Ser Gly
 290 295

<210> 79
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> conserved domain in prokaryotes and prokaryotes

<220>
 <221> MISC_FEATURE
 <222> 3, 4
 <223> Any amino acid

<220>
 <221> MISC_FEATURE
 <222> 6
 <223> Gly or Ala

<400> 79

Arg Val Xaa Xaa Gly Xaa Ser
 1 5

<210> 80
 <211> 630
 <212> DNA
 <213> Oncorhynchus mykiss

<400> 80
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 gggccccgac tccagcatca cagacaggct ggaccaccct gtgctgcatg tgatcatggca 120
 ggacgctgtg gcctactgct cctgggccta caagagacta cccacagagg ctgagtggga 180

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gtacgcctgc agagggggcc tacaggagag actttacccg tgggggaaca aactgaaacc 240
taaaggacag cactacgcca acctctggca gggaaagtcc cccacacaca actcagaaga 300
ggacgggtac actaaaacct caccagtga gtcatttcct gcaaattggct atggcctgta 360
caacatggta gggaatgcat gggagtggac atctgactgg tggactgtac accacaccac 420
agatgaacag cacaaccgg caggtccacc atcaggcaca gaccgagtga agaaaggagg 480
ctcctacatg tgccataagt catactgtta caggtacagg tgtgcagcac ggagtcagaa 540
caccctgac agctctgcct ctaacctagg gttccgctgt gtctcccagg agcagccgta 600
acctttcacc ctgcaccctg acatgggtag 630

```

```

<210> 81
<211> 655
<212> DNA
<213> Danio rerio

```

```

<220>
<221> misc_feature
<222> 590
<223> n is a, c, g, or t

```

```

<220>
<221> misc_feature
<222> 626
<223> n is a, c, g, or t

```

```

<400> 81
caaattggttt tatttacata aaaaaatcct cttagtttga agtgtaagac agtgagatta 60
gtgatgtttg aggttatgga tcaacatcag aggcgcagcg gaagcccaag ttcgaggctg 120
aactgtccgg tgtgttctga ctgcgagcgg cacacctgta tctgtagcag taagacttgt 180
ggcacatgta ggatcctcct ttcttgactc tgtctgtccc tgattctggg ccctttgggt 240
taaacttgtc ttctgcagtg tgatgcacag tccaccagtc tgccgtccac tcccacgcat 300
ttcccacat gtcatacagg ccaaagccat tgggaggaaa agacatcacc ggggatgtgt 360
tggcatagcc gtcctctgca gtgttgat tagggaaatc tccctgccac aggttagcat 420
agtgtgccc tcttggcatt aatttatctc cccatgggta catcctgtcc tgtagtctc 480
ctctacaggc caactcccat tcagcttctg taggaagtct gcgtttggcc cattgacagt 540
acgcccgtgc atcatcccat gaaacatgca gagcagggtg attcattctn gtgtgtatgg 600
ttgaatctgg tcctttctgg tgtctncagt ctgcaccttt cactgggtgac cacca 655

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<210> 82
 <211> 773
 <212> DNA
 <213> *Oryzias latipes*

<220>
 <221> misc_feature
 <222> 690
 <223> n is a, c, g, or t

<220>
 <221> misc_feature
 <222> 755
 <223> n is a, c, g, or t

<400> 82
 tctccttttt tccataaata acattagagt ccttacattc tgcctttaca tacattgtca 60
 gagacagtac aaaaaatctg cctttgtaaa attagagtta caaaaatata ttttagattt 120
 gactttcttca gaattgtcgg tggcagcaaa agaatcggat tgatctcatg acaagagcgt 180
 gagccagaag ttcttggatc aaactgattt ggttctgtca tcgtttctgt tcagcagcac 240
 agcgaaaacc aagattggaa gcggagctgt ctggagtgtt ttggcttcga gcagcacatc 300
 tgtacctgta acaataagac ttgtggcaca tgtacgagcc tcctttcttc accttatctg 360
 tgcctgacgg aggaccctgt gggttgtgct gatggtctgt tgtgtggtgc acgctccacc 420
 agtctgaggt cactcccat gcgttcccca ccatgtcata cagacaaaa gcattgcctg 480
 ggaaggacat caccggggag gtttttagtgt agccatcttc tgcagagttg tgtgctggga 540
 attccccctg ccagagggtg gcgtaatgct gtccctttgg gtttagcttg tttccccagg 600
 ggtagagtct gtccttcagg ccgcccctgc aggcaacctc cactctgcc tcagtgggaa 660
 gtctcttggt gaccaggag cagtaagcnn aggcattcatt ccagaaaacc tgaacgacgg 720
 atgatccatc ctgtctgtga tggtggagtc tggancttca gggtgcttcc agt 773

<210> 83
 <211> 566
 <212> DNA
 <213> *Xenopus laevis*

<220>
 <221> misc_feature
 <222> 6
 <223> n is a, c, g, or t

<220>

<221> misc_feature
 <222> 47
 <223> n is a, c, g, or t

<220>
 <221> misc_feature
 <222> 81
 <223> n is a, c, g, or t

<400> 83
 atatgnaact aaaggtaatg taattggaat gatggatttc acaaggntcg agagttccct 60
 attgctcctg cttgtcgtgt nacaggtcac ggagccggcg ccacacagcg aaatcccagg 120
 ttggaggccg agctgtcggg tgtattctga cttcgagcag cacagcgata cctgtagcaa 180
 taggactcat ggcacatgta ggagcctcct ttcttcactc tatcatttcc cgtagaaggt 240
 cctttcgggt tgtgaacctc atctgctgta tgatgagtgt cccaccaatc agatgtccac 300
 tcccaagcat ttcccaccat gttatataga ccataaccat tggctgggaa agcagttaca 360
 ggtgaagtct gcacataacc atcctctcca gtgttttggg ttggaaaatc cccctgccag 420
 acattcgcat aatgttgtcc ctttggttcc agcttggtcc cccatggaaa aatcctgttc 480
 tcaagtcccc cgcggcaggc gtattcccac tcagcttcag ttggaaggcg tttacctgcc 540
 caggtgcaga aagcagaagc atcatt 566

<210> 84
 <211> 647
 <212> DNA
 <213> *Silurana tropicalis*

<400> 84
 gccgcttttt tttttttttt tttttttttt catcacaaaa ataattttat taataaaata 60
 ggattttgtg ttcattctta ttatgaagga caaggaatgt cattgaaatt tttgttttca 120
 caaggtcttg ggagttcctt cctgctcagg tcattttgca gtggtcacgg agccgacgcc 180
 acgcagcgga atcccagggt agaggccgag ctgtcaggtg tattctgact tcgagcagca 240
 cagcgatacc tgtagcagta ggactcatgg cacatgtatg agcctccttt tttcaccttg 300
 tcttttcccg taaaaggacc tttcgggttg taagtctcat ctgctgtatg atgagtgtcc 360
 caccaatcgg atgtccactc ccaagcattt cccaccatgt tatataggct ataaccattg 420
 gctgggaaag cggttacagg tgaagtctgc acatagccgt cctctccagt gttttgggtt 480
 ggaaattccc cctgccagac attcgcataa tgttctccct ttggttccag cttgttcccc 540
 cacggaaaaa gcctgttctc aagtccccca cgggaggcat attcccactc agcttctgtc 600

ggaaggcgct tacccgcccc ggtgcagaag gcagaagcat cgttcca 647

<210> 85
 <211> 636
 <212> DNA
 <213> Salmo salar

<400> 85
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 ggtaatcctg catttcatga agaacactga catcactggc tgtatgaaga ggtgcacttg 120
 atttgtttcg cctggcgggc aagataggca gagtttagcac cctagactag agccaatggc 180
 gaatggtaca aaaagggaaa agtcagacta cccatgtcag ggtcaagggt aaaagggttac 240
 ggctgctcct gggagacaca gcggaaccct aggttagagg cagagctgtc aggggtgttc 300
 tgactccgtg ctgcacacct gtacctgtaa cagtatgact tatggcacat gtaggagcct 360
 cctttcttca ctcggtctgt gcctgatggg ggacctgccg ggttggtgccg ttcattctgtg 420
 gtgtggtgta cagtccacca gtcagatgtc cactcccatg cattccctac catgttgtac 480
 aggccatagc catttgcagg aaatgacttc actggtgagg ttttggtgta cccgtcctct 540
 tctgagttgt gtgtggggaa ctttcctgtc cagaggttgg cgtagtgtg tccttttaggt 600
 ttcagtttgt tccccacgg gtaaagtctg tcctgt 636

<210> 86
 <211> 415
 <212> DNA
 <213> Sus scrofa

<400> 86
 agtttctgt gaccaacacc ggagaggatg gcttccgagg aactgagcct gttgatgcct 60
 ttctcccaa tggttatggc ctttacaata tagtagggaa cgcctgggaa tggacctcag 120
 actggtggac cattcaccat gctgctgaag aaacaattaa cccatcaagt tcttctgtct 180
 gcaccgaata acagagccgc cactacgtga tgaaagcaga gaaaggcccc ctttctggga 240
 aagaccgggt gaagaaagg ggatcctata tgtgccataa gtcctactgc tacaggtacc 300
 gctgtgtgtc tcgaagccag aacacgccgg acagctcggc ttcaaactctg gggttccgct 360
 gtgcagctga ccaccagccc accacaggct gagtcaggaa gagtcttccc gaatc 415

<210> 87
 <211> 595
 <212> DNA
 <213> Bos taurus

<400> 87
ccacgcgtcc gggggcaaca aactgcagcc gaaaggccag cattatagcc aacatcttgg 60
caaggcgagt ttcctgtgac caacaccggg gaggacggct tccgagggaac cgcgcctgtt 120
gacgcctttc ctcccaatgg ttattggctt atacaatata gtagggaacg cctgggagtg 180
gacttcagac tgggtggactg ttcaccattc tgctgaagaa acgattaacc caaaaggccc 240
cccttcttggg aaagaccggg tgaagaaagg tggatcctac atgtgccata aatcctattg 300
ctacaggtat cgctgtgctg ctggaagcca gaacacaccc gacagctctg cttcgaatct 360
gggattccgt tgtgcagctg accacctgcc caccacaggc taagagccaa aaagagcctt 420
cccgaaccgg agaagtcgtg tctactctgc acgcggtctc cctcagaagg ctgaacaacc 480
tgctgtgaag aattcccacc ccaaggtggg ttacatacct tgcccagtgg ccaaaggacc 540
tatggcaaga ccaaattgct gagctgatca gcatgtgcgc tttattgggg gatgg 595

<210> 88
<211> 1611
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(1608)

<400> 88
atg cta ctg ctg tgg gtg tgg gtg gtc gca gcc ttg gcg ctg gcg gta 48
Met Leu Leu Leu Trp Val Ser Val Val Ala Ala Leu Ala Leu Ala Val
1 5 10 15
ctg gcc ccc gga gca ggg gag cag agg cgg aga gca gcc aaa gcg ccc 96
Leu Ala Pro Gly Ala Gly Glu Gln Arg Arg Arg Ala Ala Lys Ala Pro
20 25 30
aat gtg gtg ctg gtc gtg agc gac tcc ttc gat gga agg tta aca ttt 144
Asn Val Val Leu Val Val Ser Asp Ser Phe Asp Gly Arg Leu Thr Phe
35 40 45
cat cca gga agt cag gta gtg aaa ctt cct ttt atc aac ttt atg aag 192
His Pro Gly Ser Gln Val Val Lys Leu Pro Phe Ile Asn Phe Met Lys
50 55 60
aca cgt ggg act tcc ttt ctg aat gcc tac aca aac tct cca att tgt 240
Thr Arg Gly Thr Ser Phe Leu Asn Ala Tyr Thr Asn Ser Pro Ile Cys
65 70 75 80
tgc cca tca cgc gca gca atg tgg agt ggc ctc ttc act cac tta aca 288
Cys Pro Ser Arg Ala Ala Met Trp Ser Gly Leu Phe Thr His Leu Thr
85 90 95

| | |
|---|-----|
| gaa tct tgg aat aat ttt aag ggt cta gat cca aat tat aca aca tgg | 336 |
| Glu Ser Trp Asn Asn Phe Lys Gly Leu Asp Pro Asn Tyr Thr Thr Trp | |
| 100 105 110 | |
| atg gat gtc atg gag agg cat ggc tac cga aca cag aaa ttt ggg aaa | 384 |
| Met Asp Val Met Glu Arg His Gly Tyr Arg Thr Gln Lys Phe Gly Lys | |
| 115 120 125 | |
| ctg gac tat act tca gga cat cac tcc att agt aat cgt gtg gaa gcg | 432 |
| Leu Asp Tyr Thr Ser Gly His His Ser Ile Ser Asn Arg Val Glu Ala | |
| 130 135 140 | |
| tgg aca aga gat gtt gct ttc tta ctc aga caa gaa ggc agg ccc atg | 480 |
| Trp Thr Arg Asp Val Ala Phe Leu Leu Arg Gln Glu Gly Arg Pro Met | |
| 145 150 155 160 | |
| gtt aat ctt atc cgt aac agg act aaa gtc aga gtg atg gaa agg gat | 528 |
| Val Asn Leu Ile Arg Asn Arg Thr Lys Val Arg Val Met Glu Arg Asp | |
| 165 170 175 | |
| tgg cag aat aca gac aaa gca gta aac tgg tta aga aag gaa gca att | 576 |
| Trp Gln Asn Thr Asp Lys Ala Val Asn Trp Leu Arg Lys Glu Ala Ile | |
| 180 185 190 | |
| aat tac act gaa cca ttt gtt att tac ttg gga tta aat tta cca cac | 624 |
| Asn Tyr Thr Glu Pro Phe Val Ile Tyr Leu Gly Leu Asn Leu Pro His | |
| 195 200 205 | |
| cct tac cct tca cca tct tct gga gaa aat ttt gga tct tca aca ttt | 672 |
| Pro Tyr Pro Ser Pro Ser Ser Gly Glu Asn Phe Gly Ser Ser Thr Phe | |
| 210 215 220 | |
| cac aca tct ctt tat tgg ctt gaa aaa gtg tct cat gat gcc atc aaa | 720 |
| His Thr Ser Leu Tyr Trp Leu Glu Lys Val Ser His Asp Ala Ile Lys | |
| 225 230 235 240 | |
| atc cca aag tgg tca cct ttg tca gaa atg cac cct gta gat tat tac | 768 |
| Ile Pro Lys Trp Ser Pro Leu Ser Glu Met His Pro Val Asp Tyr Tyr | |
| 245 250 255 | |
| tct tct tat aca aaa aac tgc act gga aga ttt aca aaa aaa gaa att | 816 |
| Ser Ser Tyr Thr Lys Asn Cys Thr Gly Arg Phe Thr Lys Lys Glu Ile | |
| 260 265 270 | |
| aag aat att aga gca ttt tat tat gct atg tgt gct gag aca gat gcc | 864 |
| Lys Asn Ile Arg Ala Phe Tyr Tyr Ala Met Cys Ala Glu Thr Asp Ala | |
| 275 280 285 | |
| atg ctt ggt gaa att att ttg gcc ctt cat caa tta gat ctt ctt cag | 912 |
| Met Leu Gly Glu Ile Ile Leu Ala Leu His Gln Leu Asp Leu Leu Gln | |
| 290 295 300 | |
| aaa act att gtc ata tac tcc tca gac cat gga gag ctg gcc atg gaa | 960 |
| Lys Thr Ile Val Ile Tyr Ser Ser Asp His Gly Glu Leu Ala Met Glu | |
| 305 310 315 320 | |

| | |
|---|------|
| cat cga cag ttt tat aaa atg agc atg tac gag gct agt gca cat gtt | 1008 |
| His Arg Gln Phe Tyr Lys Met Ser Met Tyr Glu Ala Ser Ala His Val | |
| 325 330 335 | |
| ccg ctt ttg atg atg gga cca gga att aaa gcc ggc cta caa gta tca | 1056 |
| Pro Leu Leu Met Met Gly Pro Gly Ile Lys Ala Gly Leu Gln Val Ser | |
| 340 345 350 | |
| aat gtg gtt tct ctt gtg gat att tac cct acc atg ctt gat att gct | 1104 |
| Asn Val Val Ser Leu Val Asp Ile Tyr Pro Thr Met Leu Asp Ile Ala | |
| 355 360 365 | |
| gga att cct ctg cct cag aac ctg agt gga tac tct ttg ttg ccg tta | 1152 |
| Gly Ile Pro Leu Pro Gln Asn Leu Ser Gly Tyr Ser Leu Leu Pro Leu | |
| 370 375 380 | |
| tca tca gaa aca ttt aag aat gaa cat aaa gtc aaa aac ctg cat cca | 1200 |
| Ser Ser Glu Thr Phe Lys Asn Glu His Lys Val Lys Asn Leu His Pro | |
| 385 390 395 400 | |
| ccc tgg att ctg agt gaa ttc cat gga tgt aat gtg aat gcc tcc acc | 1248 |
| Pro Trp Ile Leu Ser Glu Phe His Gly Cys Asn Val Asn Ala Ser Thr | |
| 405 410 415 | |
| tac atg ctt cga act aac cac tgg aaa tat ata gcc tat tcg gat ggt | 1296 |
| Tyr Met Leu Arg Thr Asn His Trp Lys Tyr Ile Ala Tyr Ser Asp Gly | |
| 420 425 430 | |
| gca tca ata ttg cct caa ctc ttt gat ctt tcc tcg gat cca gat gaa | 1344 |
| Ala Ser Ile Leu Pro Gln Leu Phe Asp Leu Ser Ser Asp Pro Asp Glu | |
| 435 440 445 | |
| tta aca aat gtt gct gta aaa ttt cca gaa att act tat tct ttg gat | 1392 |
| Leu Thr Asn Val Ala Val Lys Phe Pro Glu Ile Thr Tyr Ser Leu Asp | |
| 450 455 460 | |
| cag aag ctt cat tcc att ata aac tac cct aaa gtt tct gct tct gtc | 1440 |
| Gln Lys Leu His Ser Ile Ile Asn Tyr Pro Lys Val Ser Ala Ser Val | |
| 465 470 475 480 | |
| cac cag tat aat aaa gag cag ttt atc aag tgg aaa caa agt ata gga | 1488 |
| His Gln Tyr Asn Lys Glu Gln Phe Ile Lys Trp Lys Gln Ser Ile Gly | |
| 485 490 495 | |
| cag aat tat tca aac gtt ata gca aat ctt agg tgg cac caa gac tgg | 1536 |
| Gln Asn Tyr Ser Asn Val Ile Ala Asn Leu Arg Trp His Gln Asp Trp | |
| 500 505 510 | |
| cag aag gaa cca agg aag tat gaa aat gca att gat cag tgg ctt aaa | 1584 |
| Gln Lys Glu Pro Arg Lys Tyr Glu Asn Ala Ile Asp Gln Trp Leu Lys | |
| 515 520 525 | |
| acc cat atg aat cca aga gca gtt tga | 1611 |
| Thr His Met Asn Pro Arg Ala Val | |
| 530 535 | |

<210> 89
 <211> 536
 <212> PRT
 <213> Homo sapiens

<400> 89

Met Leu Leu Leu Trp Val Ser Val Val Ala Ala Leu Ala Leu Ala Val
 1 5 10 15

Leu Ala Pro Gly Ala Gly Glu Gln Arg Arg Arg Ala Ala Lys Ala Pro
 20 25 30

Asn Val Val Leu Val Val Ser Asp Ser Phe Asp Gly Arg Leu Thr Phe
 35 40 45

His Pro Gly Ser Gln Val Val Lys Leu Pro Phe Ile Asn Phe Met Lys
 50 55 60

Thr Arg Gly Thr Ser Phe Leu Asn Ala Tyr Thr Asn Ser Pro Ile Cys
 65 70 75 80

Cys Pro Ser Arg Ala Ala Met Trp Ser Gly Leu Phe Thr His Leu Thr
 85 90 95

Glu Ser Trp Asn Asn Phe Lys Gly Leu Asp Pro Asn Tyr Thr Thr Trp
 100 105 110

Met Asp Val Met Glu Arg His Gly Tyr Arg Thr Gln Lys Phe Gly Lys
 115 120 125

Leu Asp Tyr Thr Ser Gly His His Ser Ile Ser Asn Arg Val Glu Ala
 130 135 140

Trp Thr Arg Asp Val Ala Phe Leu Leu Arg Gln Glu Gly Arg Pro Met
 145 150 155 160

Val Asn Leu Ile Arg Asn Arg Thr Lys Val Arg Val Met Glu Arg Asp
 165 170 175

Trp Gln Asn Thr Asp Lys Ala Val Asn Trp Leu Arg Lys Glu Ala Ile
 180 185 190

Asn Tyr Thr Glu Pro Phe Val Ile Tyr Leu Gly Leu Asn Leu Pro His
 195 200 205

Pro Tyr Pro Ser Pro Ser Ser Gly Glu Asn Phe Gly Ser Ser Thr Phe
 210 215 220

His Thr Ser Leu Tyr Trp Leu Glu Lys Val Ser His Asp Ala Ile Lys
 225 230 235 240

Ile Pro Lys Trp Ser Pro Leu Ser Glu Met His Pro Val Asp Tyr Tyr
 245 250 255

Ser Ser Tyr Thr Lys Asn Cys Thr Gly Arg Phe Thr Lys Lys Glu Ile
 260 265 270

Lys Asn Ile Arg Ala Phe Tyr Tyr Ala Met Cys Ala Glu Thr Asp Ala
 275 280 285

Met Leu Gly Glu Ile Ile Leu Ala Leu His Gln Leu Asp Leu Leu Gln
 290 295 300

Lys Thr Ile Val Ile Tyr Ser Ser Asp His Gly Glu Leu Ala Met Glu
 305 310 315 320

His Arg Gln Phe Tyr Lys Met Ser Met Tyr Glu Ala Ser Ala His Val
 325 330 335

Pro Leu Leu Met Met Gly Pro Gly Ile Lys Ala Gly Leu Gln Val Ser
 340 345 350

Asn Val Val Ser Leu Val Asp Ile Tyr Pro Thr Met Leu Asp Ile Ala
 355 360 365

Gly Ile Pro Leu Pro Gln Asn Leu Ser Gly Tyr Ser Leu Leu Pro Leu
 370 375 380

Ser Ser Glu Thr Phe Lys Asn Glu His Lys Val Lys Asn Leu His Pro
 385 390 395 400

Pro Trp Ile Leu Ser Glu Phe His Gly Cys Asn Val Asn Ala Ser Thr
 405 410 415

Tyr Met Leu Arg Thr Asn His Trp Lys Tyr Ile Ala Tyr Ser Asp Gly
 420 425 430

Ala Ser Ile Leu Pro Gln Leu Phe Asp Leu Ser Ser Asp Pro Asp Glu
435 440 445

Leu Thr Asn Val Ala Val Lys Phe Pro Glu Ile Thr Tyr Ser Leu Asp
450 455 460

Gln Lys Leu His Ser Ile Ile Asn Tyr Pro Lys Val Ser Ala Ser Val
465 470 475 480

His Gln Tyr Asn Lys Glu Gln Phe Ile Lys Trp Lys Gln Ser Ile Gly
485 490 495

Gln Asn Tyr Ser Asn Val Ile Ala Asn Leu Arg Trp His Gln Asp Trp
500 505 510

Gln Lys Glu Pro Arg Lys Tyr Glu Asn Ala Ile Asp Gln Trp Leu Lys
515 520 525

Thr His Met Asn Pro Arg Ala Val
530 535

<210> 90
<211> 1722
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(1719)

| | |
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| <400> 90 | |
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| Met Gly Ala Leu Ala Gly Phe Trp Ile Leu Cys Leu Leu Thr Tyr Gly | |
| 1 5 10 15 | |
| tac ctg tcc tgg ggc cag gcc tta gaa gag gag gaa gaa ggg gcc tta | 96 |
| Tyr Leu Ser Trp Gly Gln Ala Leu Glu Glu Glu Glu Glu Gly Ala Leu | |
| 20 25 30 | |
| cta gct caa gct gga gag aaa cta gag ccc agc aca act tcc acc tcc | 144 |
| Leu Ala Gln Ala Gly Glu Lys Leu Glu Pro Ser Thr Thr Ser Thr Ser | |
| 35 40 45 | |
| cag ccc cat ctc att ttc atc cta gcg gat gat cag gga ttt aga gat | 192 |
| Gln Pro His Leu Ile Phe Ile Leu Ala Asp Asp Gln Gly Phe Arg Asp | |
| 50 55 60 | |
| gtg ggt tac cac gga tct gag att aaa aca cct act ctt gac aag ctc | 240 |

| | | | | | | | | | | | | | | | | |
|-----------|-----|-----|-----|-----|-----------|-----|-----|-----|-----|-----------|-----|-----|-----|-----|-----------|-----|
| Val 65 | Gly | Tyr | His | Gly | Ser 70 | Glu | Ile | Lys | Thr | Pro 75 | Thr | Leu | Asp | Lys | Leu 80 | |
| gct | gcc | gaa | gga | gtt | aaa | ctg | gag | aac | tac | tat | gtc | cag | cct | att | tgc | 288 |
| Ala | Ala | Glu | Gly | Val | Lys | Leu | Glu | Asn | Tyr | Tyr | Val | Gln | Pro | Ile | Cys | |
| | | | | 85 | | | | 90 | | | | | | 95 | | |
| aca | cca | tcc | agg | agt | cag | ttt | att | act | gga | aag | tat | cag | ata | cac | acc | 336 |
| Thr | Pro | Ser | Arg | Ser | Gln | Phe | Ile | Thr | Gly | Lys | Tyr | Gln | Ile | His | Thr | |
| | | | 100 | | | | | 105 | | | | | 110 | | | |
| gga | ctt | caa | cat | tct | atc | ata | aga | cct | acc | caa | ccc | aac | tgt | tta | cct | 384 |
| Gly | Leu | Gln | His | Ser | Ile | Ile | Arg | Pro | Thr | Gln | Pro | Asn | Cys | Leu | Pro | |
| | | 115 | | | | | 120 | | | | | 125 | | | | |
| ctg | gac | aat | gcc | acc | cta | cct | cag | aaa | ctg | aag | gag | gtt | gga | tat | tca | 432 |
| Leu | Asp | Asn | Ala | Thr | Leu | Pro | Gln | Lys | Leu | Lys | Glu | Val | Gly | Tyr | Ser | |
| | 130 | | | | | 135 | | | | | 140 | | | | | |
| acg | cat | atg | gtc | gga | aaa | tgg | cac | ttg | ggt | ttt | tac | aga | aaa | gaa | tgc | 480 |
| Thr | His | Met | Val | Gly | Lys | Trp | His | Leu | Gly | Phe | Tyr | Arg | Lys | Glu | Cys | |
| 145 | | | | | 150 | | | | 155 | | | | | 160 | | |
| atg | ccc | acc | aga | aga | gga | ttt | gat | acc | ttt | ttt | ggt | tcc | ctt | ttg | gga | 528 |
| Met | Pro | Thr | Arg | Arg | Gly | Phe | Asp | Thr | Phe | Phe | Gly | Ser | Leu | Leu | Gly | |
| | | | | 165 | | | | 170 | | | | | 175 | | | |
| agt | ggg | gat | tac | tat | aca | cac | tac | aaa | tgt | gac | agt | cct | ggg | atg | tgt | 576 |
| Ser | Gly | Asp | Tyr | Tyr | Thr | His | Tyr | Lys | Cys | Asp | Ser | Pro | Gly | Met | Cys | |
| | | | 180 | | | | | 185 | | | | | 190 | | | |
| ggc | tat | gac | ttg | tat | gaa | aac | gac | aat | gct | gcc | tgg | gac | tat | gac | aat | 624 |
| Gly | Tyr | Asp | Leu | Tyr | Glu | Asn | Asp | Asn | Ala | Ala | Trp | Asp | Tyr | Asp | Asn | |
| | | 195 | | | | 200 | | | | | | 205 | | | | |
| ggc | ata | tac | tcc | aca | cag | atg | tac | act | cag | aga | gta | cag | caa | atc | tta | 672 |
| Gly | Ile | Tyr | Ser | Thr | Gln | Met | Tyr | Thr | Gln | Arg | Val | Gln | Gln | Ile | Leu | |
| | 210 | | | | | 215 | | | | | 220 | | | | | |
| gct | tcc | cat | aac | ccc | aca | aag | cct | ata | ttt | tta | tat | att | gcc | tat | caa | 720 |
| Ala | Ser | His | Asn | Pro | Thr | Lys | Pro | Ile | Phe | Leu | Tyr | Ile | Ala | Tyr | Gln | |
| 225 | | | | 230 | | | | 235 | | | | | | 240 | | |
| gct | gtt | cat | tca | cca | ctg | caa | gct | cct | ggc | agg | tat | ttc | gaa | cac | tac | 768 |
| Ala | Val | His | Ser | Pro | Leu | Gln | Ala | Pro | Gly | Arg | Tyr | Phe | Glu | His | Tyr | |
| | | | | 245 | | | | 250 | | | | | 255 | | | |
| cga | tcc | att | atc | aac | ata | aac | agg | agg | aga | tat | gct | gcc | atg | ctt | tcc | 816 |
| Arg | Ser | Ile | Ile | Asn | Ile | Asn | Arg | Arg | Arg | Tyr | Ala | Ala | Met | Leu | Ser | |
| | | | 260 | | | | 265 | | | | | 270 | | | | |
| tgc | tta | gat | gaa | gca | atc | aac | aac | gtg | aca | ttg | gct | cta | aag | act | tat | 864 |
| Cys | Leu | Asp | Glu | Ala | Ile | Asn | Asn | Val | Thr | Leu | Ala | Leu | Lys | Thr | Tyr | |
| | | 275 | | | | 280 | | | | | 285 | | | | | |
| ggt | ttc | tat | aac | aac | agc | att | atc | att | tac | tct | tca | gat | aat | ggt | ggc | 912 |
| Gly | Phe | Tyr | Asn | Asn | Ser | Ile | Ile | Ile | Tyr | Ser | Ser | Asp | Asn | Gly | Gly | |

| 290 | 295 | 300 | |
|---|-----|-----|------|
| cag cct acg gca gga ggg agt aac tgg cct ctc aga ggt agc aaa gga Gln Pro Thr Ala Gly Gly Ser Asn Trp Pro Leu Arg Gly Ser Lys Gly 305 310 315 320 | | | 960 |
| aca tat tgg gaa gga ggg atc cgg gct gta ggc ttt gtg cat agc cca Thr Tyr Trp Glu Gly Gly Ile Arg Ala Val Gly Phe Val His Ser Pro 325 330 335 | | | 1008 |
| ctt ctg aaa aac aag gga aca gtg tgt aag gaa ctt gtg cac atc act Leu Leu Lys Asn Lys Gly Thr Val Cys Lys Glu Leu Val His Ile Thr 340 345 350 | | | 1056 |
| gac tgg tac ccc act ctc att tca ctg gct gaa gga cag att gat gag Asp Trp Tyr Pro Thr Leu Ile Ser Leu Ala Glu Gly Gln Ile Asp Glu 355 360 365 | | | 1104 |
| gac att caa cta gat ggc tat gat atc tgg gag acc ata agt gag ggt Asp Ile Gln Leu Asp Gly Tyr Asp Ile Trp Glu Thr Ile Ser Glu Gly 370 375 380 | | | 1152 |
| ctt cgc tca ccc cga gta gat att ttg cat aac att gac ccc ata tac Leu Arg Ser Pro Arg Val Asp Ile Leu His Asn Ile Asp Pro Ile Tyr 385 390 395 400 | | | 1200 |
| acc aag gca aaa aat ggc tcc tgg gca gca ggc tat ggg atc tgg aac Thr Lys Ala Lys Asn Gly Ser Trp Ala Ala Gly Tyr Gly Ile Trp Asn 405 410 415 | | | 1248 |
| act gca atc cag tca gcc atc aga gtg cag cac tgg aaa ttg ctt aca Thr Ala Ile Gln Ser Ala Ile Arg Val Gln His Trp Lys Leu Leu Thr 420 425 430 | | | 1296 |
| gga aat cct ggc tac agc gac tgg gtc ccc cct cag tct ttc agc aac Gly Asn Pro Gly Tyr Ser Asp Trp Val Pro Pro Gln Ser Phe Ser Asn 435 440 445 | | | 1344 |
| ctg gga ccg aac cgg tgg cac aat gaa cgg atc acc ttg tca act ggc Leu Gly Pro Asn Arg Trp His Asn Glu Arg Ile Thr Leu Ser Thr Gly 450 455 460 | | | 1392 |
| aaa agt gta tgg ctt ttc aac atc aca gcc gac cca tat gag agg gtg Lys Ser Val Trp Leu Phe Asn Ile Thr Ala Asp Pro Tyr Glu Arg Val 465 470 475 480 | | | 1440 |
| gac cta tct aac agg tat cca gga atc gtg aag aag ctc cta cgg agg Asp Leu Ser Asn Arg Tyr Pro Gly Ile Val Lys Lys Leu Leu Arg Arg 485 490 495 | | | 1488 |
| ctc tca cag ttc aac aaa act gca gtg ccg gtc agg tat ccc ccc aaa Leu Ser Gln Phe Asn Lys Thr Ala Val Pro Val Arg Tyr Pro Pro Lys 500 505 510 | | | 1536 |
| gac ccc aga agt aac cct agg ctc aat gga ggg gtc tgg gga cca tgg Asp Pro Arg Ser Asn Pro Arg Leu Asn Gly Gly Val Trp Gly Pro Trp 515 520 525 | | | 1584 |

tat aaa gag gaa acc aag aaa aag aag cca agc aaa aat cag gct gag 1632
 Tyr Lys Glu Glu Thr Lys Lys Lys Lys Pro Ser Lys Asn Gln Ala Glu
 530 535 540

aaa aag caa aag aaa agc aaa aaa aag aag aag aaa cag cag aaa gca 1680
 Lys Lys Gln Lys Lys Ser Lys Lys Lys Lys Lys Lys Gln Gln Lys Ala
 545 550 555 560

gtc tca ggt tca act tgc cat tca ggt gtt act tgt gga taa 1722
 Val Ser Gly Ser Thr Cys His Ser Gly Val Thr Cys Gly
 565 570

<210> 91
 <211> 573
 <212> PRT
 <213> Homo sapiens

<400> 91

Met Gly Ala Leu Ala Gly Phe Trp Ile Leu Cys Leu Leu Thr Tyr Gly
 1 5 10 15

Tyr Leu Ser Trp Gly Gln Ala Leu Glu Glu Glu Glu Gly Ala Leu
 20 25 30

Leu Ala Gln Ala Gly Glu Lys Leu Glu Pro Ser Thr Thr Ser Thr Ser
 35 40 45

Gln Pro His Leu Ile Phe Ile Leu Ala Asp Asp Gln Gly Phe Arg Asp
 50 55 60

Val Gly Tyr His Gly Ser Glu Ile Lys Thr Pro Thr Leu Asp Lys Leu
 65 70 75 80

Ala Ala Glu Gly Val Lys Leu Glu Asn Tyr Tyr Val Gln Pro Ile Cys
 85 90 95

Thr Pro Ser Arg Ser Gln Phe Ile Thr Gly Lys Tyr Gln Ile His Thr
 100 105 110

Gly Leu Gln His Ser Ile Ile Arg Pro Thr Gln Pro Asn Cys Leu Pro
 115 120 125

Leu Asp Asn Ala Thr Leu Pro Gln Lys Leu Lys Glu Val Gly Tyr Ser
 130 135 140

Thr His Met Val Gly Lys Trp His Leu Gly Phe Tyr Arg Lys Glu Cys
145 150 155 160

Met Pro Thr Arg Arg Gly Phe Asp Thr Phe Phe Gly Ser Leu Leu Gly
165 170 175

Ser Gly Asp Tyr Tyr Thr His Tyr Lys Cys Asp Ser Pro Gly Met Cys
180 185 190

Gly Tyr Asp Leu Tyr Glu Asn Asp Asn Ala Ala Trp Asp Tyr Asp Asn
195 200 205

Gly Ile Tyr Ser Thr Gln Met Tyr Thr Gln Arg Val Gln Gln Ile Leu
210 215 220

Ala Ser His Asn Pro Thr Lys Pro Ile Phe Leu Tyr Ile Ala Tyr Gln
225 230 235 240

Ala Val His Ser Pro Leu Gln Ala Pro Gly Arg Tyr Phe Glu His Tyr
245 250 255

Arg Ser Ile Ile Asn Ile Asn Arg Arg Arg Tyr Ala Ala Met Leu Ser
260 265 270

Cys Leu Asp Glu Ala Ile Asn Asn Val Thr Leu Ala Leu Lys Thr Tyr
275 280 285

Gly Phe Tyr Asn Asn Ser Ile Ile Ile Tyr Ser Ser Asp Asn Gly Gly
290 295 300

Gln Pro Thr Ala Gly Gly Ser Asn Trp Pro Leu Arg Gly Ser Lys Gly
305 310 315 320

Thr Tyr Trp Glu Gly Gly Ile Arg Ala Val Gly Phe Val His Ser Pro
325 330 335

Leu Leu Lys Asn Lys Gly Thr Val Cys Lys Glu Leu Val His Ile Thr
340 345 350

Asp Trp Tyr Pro Thr Leu Ile Ser Leu Ala Glu Gly Gln Ile Asp Glu
355 360 365

Asp Ile Gln Leu Asp Gly Tyr Asp Ile Trp Glu Thr Ile Ser Glu Gly

370

375

380

Leu Arg Ser Pro Arg Val Asp Ile Leu His Asn Ile Asp Pro Ile Tyr
 385 390 395 400

Thr Lys Ala Lys Asn Gly Ser Trp Ala Ala Gly Tyr Gly Ile Trp Asn
 405 410 415

Thr Ala Ile Gln Ser Ala Ile Arg Val Gln His Trp Lys Leu Leu Thr
 420 425 430

Gly Asn Pro Gly Tyr Ser Asp Trp Val Pro Pro Gln Ser Phe Ser Asn
 435 440 445

Leu Gly Pro Asn Arg Trp His Asn Glu Arg Ile Thr Leu Ser Thr Gly
 450 455 460

Lys Ser Val Trp Leu Phe Asn Ile Thr Ala Asp Pro Tyr Glu Arg Val
 465 470 475 480

Asp Leu Ser Asn Arg Tyr Pro Gly Ile Val Lys Lys Leu Leu Arg Arg
 485 490 495

Leu Ser Gln Phe Asn Lys Thr Ala Val Pro Val Arg Tyr Pro Pro Lys
 500 505 510

Asp Pro Arg Ser Asn Pro Arg Leu Asn Gly Gly Val Trp Gly Pro Trp
 515 520 525

Tyr Lys Glu Glu Thr Lys Lys Lys Lys Pro Ser Lys Asn Gln Ala Glu
 530 535 540

Lys Lys Gln Lys Lys Ser Lys Lys Lys Lys Lys Lys Gln Gln Lys Ala
 545 550 555 560

Val Ser Gly Ser Thr Cys His Ser Gly Val Thr Cys Gly
 565 570

<210> 92
 <211> 1710
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1707)

<400> 92

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| atg cac acc ctc act ggc ttc tcc ctg gtc agc ctg ctc agc ttc ggc | 48 |
| Met His Thr Leu Thr Gly Phe Ser Leu Val Ser Leu Leu Ser Phe Gly | |
| 1 5 10 15 | |
| tac ctg tcc tgg gac tgg gcc aag ccg agc ttc gtg gcc gac ggg ccc | 96 |
| Tyr Leu Ser Trp Asp Trp Ala Lys Pro Ser Phe Val Ala Asp Gly Pro | |
| 20 25 30 | |
| ggg gag gct ggc gag cag ccc tcg gcc gct ccg ccc cag cct ccc cac | 144 |
| Gly Glu Ala Gly Glu Gln Pro Ser Ala Ala Pro Pro Gln Pro Pro His | |
| 35 40 45 | |
| atc atc ttc atc ctc acg gac gac caa ggc tac cac gac gtg ggc tac | 192 |
| Ile Ile Phe Ile Leu Thr Asp Asp Gln Gly Tyr His Asp Val Gly Tyr | |
| 50 55 60 | |
| cat ggt tca gat atc gag acc cct acg ctg gac agg ctg gcg gcc aag | 240 |
| His Gly Ser Asp Ile Glu Thr Pro Thr Leu Asp Arg Leu Ala Ala Lys | |
| 65 70 75 80 | |
| ggg gtc aag ttg gag aat tat tac atc cag ccc atc tgc acg cct tcg | 288 |
| Gly Val Lys Leu Glu Asn Tyr Tyr Ile Gln Pro Ile Cys Thr Pro Ser | |
| 85 90 95 | |
| cgg agc cag ctc ctc act ggc agg tac cag atc cac aca gga ctc cag | 336 |
| Arg Ser Gln Leu Leu Thr Gly Arg Tyr Gln Ile His Thr Gly Leu Gln | |
| 100 105 110 | |
| cat tcc atc atc cgc cca cag cag ccc aac tgc ctg ccc ctg gac cag | 384 |
| His Ser Ile Ile Arg Pro Gln Gln Pro Asn Cys Leu Pro Leu Asp Gln | |
| 115 120 125 | |
| gtg aca ctg cca cag aag ctg cag gag gca ggt tat tcc acc cat atg | 432 |
| Val Thr Leu Pro Gln Lys Leu Gln Glu Ala Gly Tyr Ser Thr His Met | |
| 130 135 140 | |
| gtg ggc aag tgg cac ctg ggc ttc tac cgg aag gag tgt ctg ccc acc | 480 |
| Val Gly Lys Trp His Leu Gly Phe Tyr Arg Lys Glu Cys Leu Pro Thr | |
| 145 150 155 160 | |
| cgt cgg ggc ttc gac acc ttc ctg ggc tcg ctc acg ggc aat gtg gac | 528 |
| Arg Arg Gly Phe Asp Thr Phe Leu Gly Ser Leu Thr Gly Asn Val Asp | |
| 165 170 175 | |
| tat tac acc tat gac aac tgt gat ggc cca ggc gtg tgc ggc ttc gac | 576 |
| Tyr Tyr Thr Tyr Asp Asn Cys Asp Gly Pro Gly Val Cys Gly Phe Asp | |
| 180 185 190 | |
| ctg cac gag ggt gag aat gtg gcc tgg ggg ctc agc ggc cag tac tcc | 624 |
| Leu His Glu Gly Glu Asn Val Ala Trp Gly Leu Ser Gly Gln Tyr Ser | |
| 195 200 205 | |

| | |
|---|------|
| act atg ctt tac gcc cag cgc gcc agc cat atc ctg gcc agc cac agc | 672 |
| Thr Met Leu Tyr Ala Gln Arg Ala Ser His Ile Leu Ala Ser His Ser | |
| 210 215 220 | |
| cct cag cgt ccc ctc ttc ctc tat gtg gcc ttc cag gca gta cac aca | 720 |
| Pro Gln Arg Pro Leu Phe Leu Tyr Val Ala Phe Gln Ala Val His Thr | |
| 225 230 235 240 | |
| ccc ctg cag tcc cct cgt gag tac ctg tac cgc tac cgc acc atg ggc | 768 |
| Pro Leu Gln Ser Pro Arg Glu Tyr Leu Tyr Arg Tyr Arg Thr Met Gly | |
| 245 250 255 | |
| aat gtg gcc cgg cgg aag tac gcg gcc atg gtg acc tgc atg gat gag | 816 |
| Asn Val Ala Arg Arg Lys Tyr Ala Ala Met Val Thr Cys Met Asp Glu | |
| 260 265 270 | |
| gct gtg cgc aac atc acc tgg gcc ctc aag cgc tac ggt ttc tac aac | 864 |
| Ala Val Arg Asn Ile Thr Trp Ala Leu Lys Arg Tyr Gly Phe Tyr Asn | |
| 275 280 285 | |
| aac agt gtc atc atc ttc tcc agt gac aat ggt ggc cag act ttc tcg | 912 |
| Asn Ser Val Ile Ile Phe Ser Ser Asp Asn Gly Gly Gln Thr Phe Ser | |
| 290 295 300 | |
| ggg ggc agc aac tgg ccg ctc cga gga cgc aag ggc act tat tgg gaa | 960 |
| Gly Gly Ser Asn Trp Pro Leu Arg Gly Arg Lys Gly Thr Tyr Trp Glu | |
| 305 310 315 320 | |
| ggt ggc gtg cgg ggc cta ggc ttt gtc cac agt ccc ctg ctc aag cga | 1008 |
| Gly Gly Val Arg Gly Leu Gly Phe Val His Ser Pro Leu Leu Lys Arg | |
| 325 330 335 | |
| aag caa cgg aca agc cgg gca ctg atg cac atc act gac tgg tac ccg | 1056 |
| Lys Gln Arg Thr Ser Arg Ala Leu Met His Ile Thr Asp Trp Tyr Pro | |
| 340 345 350 | |
| acc ctg gtg ggt ctg gca ggt ggt acc acc tca gca gcc gat ggg cta | 1104 |
| Thr Leu Val Gly Leu Ala Gly Gly Thr Thr Ser Ala Ala Asp Gly Leu | |
| 355 360 365 | |
| gat ggc tac gac gtg tgg ccg gcc atc agc gag ggc cgg gcc tca cca | 1152 |
| Asp Gly Tyr Asp Val Trp Pro Ala Ile Ser Glu Gly Arg Ala Ser Pro | |
| 370 375 380 | |
| cgc acg gag atc ctg cac aac att gac cca ctc tac aac cat gcc cag | 1200 |
| Arg Thr Glu Ile Leu His Asn Ile Asp Pro Leu Tyr Asn His Ala Gln | |
| 385 390 395 400 | |
| cat ggc tcc ctg gag ggc ggc ttt ggc atc tgg aac acc gcc gtg cag | 1248 |
| His Gly Ser Leu Glu Gly Gly Phe Gly Ile Trp Asn Thr Ala Val Gln | |
| 405 410 415 | |
| gct gcc atc cgc gtg ggt gag tgg aag ctg ctg aca gga gac ccc ggc | 1296 |
| Ala Ala Ile Arg Val Gly Glu Trp Lys Leu Leu Thr Gly Asp Pro Gly | |
| 420 425 430 | |
| tat ggc gat tgg atc cca ccg cag aca ctg gcc acc ttc ccg ggt agc | 1344 |

Tyr Gly Asp Trp Ile Pro Pro Gln Thr Leu Ala Thr Phe Pro Gly Ser
 435 440 445
 tgg tgg aac ctg gaa cga atg gcc agt gtc cgc cag gcc gtg tgg ctc 1392
 Trp Trp Asn Leu Glu Arg Met Ala Ser Val Arg Gln Ala Val Trp Leu
 450 455 460
 ttc aac atc agt gct gac cct tat gaa cgg gag gac ctg gct ggc cag 1440
 Phe Asn Ile Ser Ala Asp Pro Tyr Glu Arg Glu Asp Leu Ala Gly Gln
 465 470 475 480
 cgg cct gat gtg gtc cgc acc ctg ctg gct cgc ctg gcc gaa tat aac 1488
 Arg Pro Asp Val Val Arg Thr Leu Leu Ala Arg Leu Ala Glu Tyr Asn
 485 490 495
 cgc aca gcc atc ccg gta cgc tac cca gct gag aac ccc cgg gct cat 1536
 Arg Thr Ala Ile Pro Val Arg Tyr Pro Ala Glu Asn Pro Arg Ala His
 500 505 510
 cct gac ttt aat ggg ggt gct tgg ggg ccc tgg gcc agt gat gag gaa 1584
 Pro Asp Phe Asn Gly Gly Ala Trp Gly Pro Trp Ala Ser Asp Glu Glu
 515 520 525
 gag gag gaa gag gaa ggg agg gct cga agc ttc tcc cgg ggt cgt cgc 1632
 Glu Glu Glu Glu Glu Gly Arg Ala Arg Ser Phe Ser Arg Gly Arg Arg
 530 535 540
 aag aaa aaa tgc aag att tgc aag ctt cga tcc ttt ttc cgt aaa ctc 1680
 Lys Lys Lys Cys Lys Ile Cys Lys Leu Arg Ser Phe Phe Arg Lys Leu
 545 550 555 560
 aac acc agg cta atg tcc caa cgg atc tga 1710
 Asn Thr Arg Leu Met Ser Gln Arg Ile
 565

<210> 93
 <211> 569
 <212> PRT
 <213> Homo sapiens

<400> 93

Met His Thr Leu Thr Gly Phe Ser Leu Val Ser Leu Leu Ser Phe Gly
 1 5 10 15

Tyr Leu Ser Trp Asp Trp Ala Lys Pro Ser Phe Val Ala Asp Gly Pro
 20 25 30

Gly Glu Ala Gly Glu Gln Pro Ser Ala Ala Pro Pro Gln Pro Pro His
 35 40 45

Ile Ile Phe Ile Leu Thr Asp Asp Gln Gly Tyr His Asp Val Gly Tyr
 50 55 60

His Gly Ser Asp Ile Glu Thr Pro Thr Leu Asp Arg Leu Ala Ala Lys
65 70 75 80

Gly Val Lys Leu Glu Asn Tyr Tyr Ile Gln Pro Ile Cys Thr Pro Ser
85 90 95

Arg Ser Gln Leu Leu Thr Gly Arg Tyr Gln Ile His Thr Gly Leu Gln
100 105 110

His Ser Ile Ile Arg Pro Gln Gln Pro Asn Cys Leu Pro Leu Asp Gln
115 120 125

Val Thr Leu Pro Gln Lys Leu Gln Glu Ala Gly Tyr Ser Thr His Met
130 135 140

Val Gly Lys Trp His Leu Gly Phe Tyr Arg Lys Glu Cys Leu Pro Thr
145 150 155 160

Arg Arg Gly Phe Asp Thr Phe Leu Gly Ser Leu Thr Gly Asn Val Asp
165 170 175

Tyr Tyr Thr Tyr Asp Asn Cys Asp Gly Pro Gly Val Cys Gly Phe Asp
180 185 190

Leu His Glu Gly Glu Asn Val Ala Trp Gly Leu Ser Gly Gln Tyr Ser
195 200 205

Thr Met Leu Tyr Ala Gln Arg Ala Ser His Ile Leu Ala Ser His Ser
210 215 220

Pro Gln Arg Pro Leu Phe Leu Tyr Val Ala Phe Gln Ala Val His Thr
225 230 235 240

Pro Leu Gln Ser Pro Arg Glu Tyr Leu Tyr Arg Tyr Arg Thr Met Gly
245 250 255

Asn Val Ala Arg Arg Lys Tyr Ala Ala Met Val Thr Cys Met Asp Glu
260 265 270

Ala Val Arg Asn Ile Thr Trp Ala Leu Lys Arg Tyr Gly Phe Tyr Asn
275 280 285

Asn Ser Val Ile Ile Phe Ser Ser Asp Asn Gly Gly Gln Thr Phe Ser
 290 295 300

Gly Gly Ser Asn Trp Pro Leu Arg Gly Arg Lys Gly Thr Tyr Trp Glu
 305 310 315 320

Gly Gly Val Arg Gly Leu Gly Phe Val His Ser Pro Leu Leu Lys Arg
 325 330 335

Lys Gln Arg Thr Ser Arg Ala Leu Met His Ile Thr Asp Trp Tyr Pro
 340 345 350

Thr Leu Val Gly Leu Ala Gly Gly Thr Thr Ser Ala Ala Asp Gly Leu
 355 360 365

Asp Gly Tyr Asp Val Trp Pro Ala Ile Ser Glu Gly Arg Ala Ser Pro
 370 375 380

Arg Thr Glu Ile Leu His Asn Ile Asp Pro Leu Tyr Asn His Ala Gln
 385 390 395 400

His Gly Ser Leu Glu Gly Gly Phe Gly Ile Trp Asn Thr Ala Val Gln
 405 410 415

Ala Ala Ile Arg Val Gly Glu Trp Lys Leu Leu Thr Gly Asp Pro Gly
 420 425 430

Tyr Gly Asp Trp Ile Pro Pro Gln Thr Leu Ala Thr Phe Pro Gly Ser
 435 440 445

Trp Trp Asn Leu Glu Arg Met Ala Ser Val Arg Gln Ala Val Trp Leu
 450 455 460

Phe Asn Ile Ser Ala Asp Pro Tyr Glu Arg Glu Asp Leu Ala Gly Gln
 465 470 475 480

Arg Pro Asp Val Val Arg Thr Leu Leu Ala Arg Leu Ala Glu Tyr Asn
 485 490 495

Arg Thr Ala Ile Pro Val Arg Tyr Pro Ala Glu Asn Pro Arg Ala His
 500 505 510

Pro Asp Phe Asn Gly Gly Ala Trp Gly Pro Trp Ala Ser Asp Glu Glu
 515 520 525

Glu Glu Glu Glu Glu Gly Arg Ala Arg Ser Phe Ser Arg Gly Arg Arg
 530 535 540

Lys Lys Lys Cys Lys Ile Cys Lys Leu Arg Ser Phe Phe Arg Lys Leu
 545 550 555 560

Asn Thr Arg Leu Met Ser Gln Arg Ile
 565

<210> 94
 <211> 2067
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(2064)

<400> 94
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 Met Leu Ile Ser Gly Arg Glu Glu Asn Gln Ile Asp Ile Ser Lys Thr
 1 5 10 15
 aca gag gta gat tgt ttt gtg gtt gaa tta gga agt cta cac aat cct 96
 Thr Glu Val Asp Cys Phe Val Val Glu Leu Gly Ser Leu His Asn Pro
 20 25 30
 aca cgg aac cca cag cga att ttc acc aag cac gtg gcc acc aag tca 144
 Thr Arg Asn Pro Gln Arg Ile Phe Thr Lys His Val Ala Thr Lys Ser
 35 40 45
 tcc agc tcc aaa tgt cag ctg gac caa ggt gga aaa agc ctg gtc cag 192
 Ser Ser Ser Lys Cys Gln Leu Asp Gln Gly Gly Lys Ser Leu Val Gln
 50 55 60
 tgc att tta ccc aga tct tca aag ctc ctc tca ccc ttg tgt ctc ccc 240
 Cys Ile Leu Pro Arg Ser Ser Lys Leu Leu Ser Pro Leu Cys Leu Pro
 65 70 75 80
 cat ccg tgt gga gct tta ctt ctg tat aga tcc tca gga atc gcc tct 288
 His Pro Cys Gly Ala Leu Leu Leu Tyr Arg Ser Ser Gly Ile Ala Ser
 85 90 95
 gct ctt gct gcc ttt aca gac tcc ctc tct agg agc tgc tgg ctg tca 336
 Ala Leu Ala Ala Phe Thr Asp Ser Leu Ser Arg Ser Cys Trp Leu Ser
 100 105 110
 gtg tcc ctg tgc tgt ttg ttt tgc ggt gtt gat ggc aca ttt atg aca 384
 Val Ser Leu Cys Cys Leu Phe Cys Gly Val Asp Gly Thr Phe Met Thr

| 115 | 120 | 125 | |
|---|-----|-----|------|
| aga aac gcc aga ccc aac att gtc ctg ctg atg gca gat gac ctt gga Arg Asn Ala Arg Pro Asn Ile Val Leu Leu Met Ala Asp Asp Leu Gly 130 135 140 | | | 432 |
| gtg ggg gat ttg tgc tgc tac ggt aat aac tca gtg agc aca cct aat Val Gly Asp Leu Cys Cys Tyr Gly Asn Asn Ser Val Ser Thr Pro Asn 145 150 155 160 | | | 480 |
| att gac cgc ctg gca agt gaa gga gtg agg ctt acc cag cat ctc gca Ile Asp Arg Leu Ala Ser Glu Gly Val Arg Leu Thr Gln His Leu Ala 165 170 175 | | | 528 |
| gct gct tcc atg tgc acc cca agt cgg gct gcc ttc ctg acc ggc cgg Ala Ala Ser Met Cys Thr Pro Ser Arg Ala Ala Phe Leu Thr Gly Arg 180 185 190 | | | 576 |
| tac ccc atc aga tca ggg atg gtg tct gcc tac aac ctg aac cgt gcc Tyr Pro Ile Arg Ser Gly Met Val Ser Ala Tyr Asn Leu Asn Arg Ala 195 200 205 | | | 624 |
| ttc acg tgg ctt ggt ggg tca ggt ggt ctt ccc acc aat gaa acg act Phe Thr Trp Leu Gly Gly Ser Gly Gly Leu Pro Thr Asn Glu Thr Thr 210 215 220 | | | 672 |
| ttt gcc aag ctg ctg cag cac cgt ggc tac cgc acg gga ctc ata ggc Phe Ala Lys Leu Leu Gln His Arg Gly Tyr Arg Thr Gly Leu Ile Gly 225 230 235 240 | | | 720 |
| aaa tgg cac ctg ggt ttg agc tgc gcc tct cgg aat gat cac tgt tac Lys Trp His Leu Gly Leu Ser Cys Ala Ser Arg Asn Asp His Cys Tyr 245 250 255 | | | 768 |
| cac ccg ctc aac cat ggt ttt cac tac ttt tac ggg gtg cct ttt gga His Pro Leu Asn His Gly Phe His Tyr Phe Tyr Gly Val Pro Phe Gly 260 265 270 | | | 816 |
| ctt tta agc gac tgc cag gca tcc aag aca cca gaa ctg cac cgc tgg Leu Leu Ser Asp Cys Gln Ala Ser Lys Thr Pro Glu Leu His Arg Trp 275 280 285 | | | 864 |
| ctc agg atc aaa ctg tgg atc tcc acg gta gcc ctt gcc ctg gtt cct Leu Arg Ile Lys Leu Trp Ile Ser Thr Val Ala Leu Ala Leu Val Pro 290 295 300 | | | 912 |
| ttt ctg ctt ctc att ccc aag ttc gcc cgc tgg ttc tca gtg cca tgg Phe Leu Leu Leu Ile Pro Lys Phe Ala Arg Trp Phe Ser Val Pro Trp 305 310 315 320 | | | 960 |
| aag gtc atc ttt gtc ttt gct ctc ctc gcc ttt ctg ttt ttc act tcc Lys Val Ile Phe Val Phe Ala Leu Leu Ala Phe Leu Phe Phe Thr Ser 325 330 335 | | | 1008 |
| tgg tac tct agt tat gga ttt act cga cgt tgg aat tgc atc ctt atg Trp Tyr Ser Ser Tyr Gly Phe Thr Arg Arg Trp Asn Cys Ile Leu Met 340 345 350 | | | 1056 |

| | |
|---|------|
| agg aac cat gaa att atc cag cag cca atg aaa gag gag aaa gta gct | 1104 |
| Arg Asn His Glu Ile Ile Gln Gln Pro Met Lys Glu Glu Lys Val Ala | |
| 355 360 365 | |
| tcc ctc atg ctg aag gag gca ctt gct ttc att gaa agg tac aaa agg | 1152 |
| Ser Leu Met Leu Lys Glu Ala Leu Ala Phe Ile Glu Arg Tyr Lys Arg | |
| 370 375 380 | |
| gaa cct ttt ctc ctc ttt ttt tcc ttc ctg cac gta cat act cca ctc | 1200 |
| Glu Pro Phe Leu Leu Phe Phe Ser Phe Leu His Val His Thr Pro Leu | |
| 385 390 395 400 | |
| atc tcc aaa aag aag ttt gtt ggg cgc agt aaa tat ggc agg tat ggg | 1248 |
| Ile Ser Lys Lys Lys Phe Val Gly Arg Ser Lys Tyr Gly Arg Tyr Gly | |
| 405 410 415 | |
| gac aat gta gaa gaa atg gat tgg atg gtg ggt aaa atc ctg gat gcc | 1296 |
| Asp Asn Val Glu Glu Met Asp Trp Met Val Gly Lys Ile Leu Asp Ala | |
| 420 425 430 | |
| ctg gac cag gag cgc ctg gcc aac cac acc ttg gtg tac ttc acc tct | 1344 |
| Leu Asp Gln Glu Arg Leu Ala Asn His Thr Leu Val Tyr Phe Thr Ser | |
| 435 440 445 | |
| gac aac ggg ggc cac ctg gag ccc ctg gac ggg gct gtt cag ctg ggt | 1392 |
| Asp Asn Gly Gly His Leu Glu Pro Leu Asp Gly Ala Val Gln Leu Gly | |
| 450 455 460 | |
| ggc tgg aac ggg atc tac aaa ggt ggc aaa gga atg gga gga tgg gaa | 1440 |
| Gly Trp Asn Gly Ile Tyr Lys Gly Gly Lys Gly Met Gly Gly Trp Glu | |
| 465 470 475 480 | |
| gga ggt atc cgt gtg cca ggg ata ttc cgg tgg ccg tca gtc ttg gag | 1488 |
| Gly Gly Ile Arg Val Pro Gly Ile Phe Arg Trp Pro Ser Val Leu Glu | |
| 485 490 495 | |
| gct ggg aga gtg atc aat gag ccc acc agc tta atg gac atc tat ccg | 1536 |
| Ala Gly Arg Val Ile Asn Glu Pro Thr Ser Leu Met Asp Ile Tyr Pro | |
| 500 505 510 | |
| acg ctg tct tat ata ggc gga ggg atc ttg tcc cag gac aga gtg att | 1584 |
| Thr Leu Ser Tyr Ile Gly Gly Gly Ile Leu Ser Gln Asp Arg Val Ile | |
| 515 520 525 | |
| gac ggc cag aac cta atg ccc ctg ctg gaa gga agg gcg tcc cac tcc | 1632 |
| Asp Gly Gln Asn Leu Met Pro Leu Leu Glu Gly Arg Ala Ser His Ser | |
| 530 535 540 | |
| gac cac gag ttc ctc ttc cac tac tgt ggg gtc tat ctg cac acg gtc | 1680 |
| Asp His Glu Phe Leu Phe His Tyr Cys Gly Val Tyr Leu His Thr Val | |
| 545 550 555 560 | |
| agg tgg cat cag aag gac tgt gca act gtg tgg aaa gct cat tat gtg | 1728 |
| Arg Trp His Gln Lys Asp Cys Ala Thr Val Trp Lys Ala His Tyr Val | |
| 565 570 575 | |

act cct aaa ttc tac cct gaa gga aca ggt gcc tgc tat ggg agt gga 1776
Thr Pro Lys Phe Tyr Pro Glu Gly Thr Gly Ala Cys Tyr Gly Ser Gly
580 585 590

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| ata | tgt | tca | tgt | tcg | ggg | gat | gta | acc | tac | cac | gac | cca | cca | ctc | ctc | 1824 |
| Ile | Cys | Ser | Cys | Ser | Gly | Asp | Val | Thr | Tyr | His | Asp | Pro | Pro | Leu | Leu | |
| | | 595 | | | | | 600 | | | | | 605 | | | | |

ttt gac atc tca aga gac cct tca gaa gcc ctt cca ctg aac cct gac 1872
Phe Asp Ile Ser Arg Asp Pro Ser Glu Ala Leu Pro Leu Asn Pro Asp
610 615 620

aat gag cca tta ttt gac tcc gtg atc aaa aag atg gag gca gcc ata 1920
Asn Glu Pro Leu Phe Asp Ser Val Ile Lys Lys Met Glu Ala Ala Ile
625 630 635 640

aga gag cat cgt agg aca cta aca cct gtc cca cag cag ttc tct gtg 1968
Arg Glu His Arg Arg Thr Leu Thr Pro Val Pro Gln Gln Phe Ser Val
645 650 655

ttc aac aca att tgg aaa cca tgg ctg cag cct tgc tgt ggg acc ttc 2016
Phe Asn Thr Ile Trp Lys Pro Trp Leu Gln Pro Cys Cys Gly Thr Phe
660 665 670

ccc ttc tgt ggg tgt gac aag gaa gat gac atc ctt ccc atg gct ccc 2064
Pro Phe Cys Gly Cys Asp Lys Glu Asp Asp Ile Leu Pro Met Ala Pro
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| tga | 2067 |
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35 40 45

Ser Ser Ser Lys Cys Gln Leu Asp Gln Gly Gly Lys Ser Leu Val Gln
50 55 60

Cys Ile Leu Pro Arg Ser Ser Lys Leu Leu Ser Pro Leu Cys Leu Pro
65 70 75 80

His Pro Cys Gly Ala Leu Leu Leu Tyr Arg Ser Ser Gly Ile Ala Ser
85 90 95

Ala Leu Ala Ala Phe Thr Asp Ser Leu Ser Arg Ser Cys Trp Leu Ser
100 105 110

Val Ser Leu Cys Cys Leu Phe Cys Gly Val Asp Gly Thr Phe Met Thr
115 120 125

Arg Asn Ala Arg Pro Asn Ile Val Leu Leu Met Ala Asp Asp Leu Gly
130 135 140

Val Gly Asp Leu Cys Cys Tyr Gly Asn Asn Ser Val Ser Thr Pro Asn
145 150 155 160

Ile Asp Arg Leu Ala Ser Glu Gly Val Arg Leu Thr Gln His Leu Ala
165 170 175

Ala Ala Ser Met Cys Thr Pro Ser Arg Ala Ala Phe Leu Thr Gly Arg
180 185 190

Tyr Pro Ile Arg Ser Gly Met Val Ser Ala Tyr Asn Leu Asn Arg Ala
195 200 205

Phe Thr Trp Leu Gly Gly Ser Gly Gly Leu Pro Thr Asn Glu Thr Thr
210 215 220

Phe Ala Lys Leu Leu Gln His Arg Gly Tyr Arg Thr Gly Leu Ile Gly
225 230 235 240

Lys Trp His Leu Gly Leu Ser Cys Ala Ser Arg Asn Asp His Cys Tyr
245 250 255

His Pro Leu Asn His Gly Phe His Tyr Phe Tyr Gly Val Pro Phe Gly
260 265 270

Leu Leu Ser Asp Cys Gln Ala Ser Lys Thr Pro Glu Leu His Arg Trp
275 280 285

Leu Arg Ile Lys Leu Trp Ile Ser Thr Val Ala Leu Ala Leu Val Pro
290 295 300

Phe Leu Leu Leu Ile Pro Lys Phe Ala Arg Trp Phe Ser Val Pro Trp
 305 310 315 320

Lys Val Ile Phe Val Phe Ala Leu Leu Ala Phe Leu Phe Phe Thr Ser
 325 330 335

Trp Tyr Ser Ser Tyr Gly Phe Thr Arg Arg Trp Asn Cys Ile Leu Met
 340 345 350

Arg Asn His Glu Ile Ile Gln Gln Pro Met Lys Glu Glu Lys Val Ala
 355 360 365

Ser Leu Met Leu Lys Glu Ala Leu Ala Phe Ile Glu Arg Tyr Lys Arg
 370 375 380

Glu Pro Phe Leu Leu Phe Phe Ser Phe Leu His Val His Thr Pro Leu
 385 390 395 400

Ile Ser Lys Lys Lys Phe Val Gly Arg Ser Lys Tyr Gly Arg Tyr Gly
 405 410 415

Asp Asn Val Glu Glu Met Asp Trp Met Val Gly Lys Ile Leu Asp Ala
 420 425 430

Leu Asp Gln Glu Arg Leu Ala Asn His Thr Leu Val Tyr Phe Thr Ser
 435 440 445

Asp Asn Gly Gly His Leu Glu Pro Leu Asp Gly Ala Val Gln Leu Gly
 450 455 460

Gly Trp Asn Gly Ile Tyr Lys Gly Gly Lys Gly Met Gly Gly Trp Glu
 465 470 475 480

Gly Gly Ile Arg Val Pro Gly Ile Phe Arg Trp Pro Ser Val Leu Glu
 485 490 495

Ala Gly Arg Val Ile Asn Glu Pro Thr Ser Leu Met Asp Ile Tyr Pro
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Thr Leu Ser Tyr Ile Gly Gly Gly Ile Leu Ser Gln Asp Arg Val Ile
 515 520 525

Asp Gly Gln Asn Leu Met Pro Leu Leu Glu Gly Arg Ala Ser His Ser

Asp Gly Gln Asn Leu Met Pro Leu Leu Glu Gly Arg Ala Ser His Ser
 530 535 540

Asp His Glu Phe Leu Phe His Tyr Cys Gly Val Tyr Leu His Thr Val
 545 550 555 560

Arg Trp His Gln Lys Asp Cys Ala Thr Val Trp Lys Ala His Tyr Val
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Thr Pro Lys Phe Tyr Pro Glu Gly Thr Gly Ala Cys Tyr Gly Ser Gly
 580 585 590

Ile Cys Ser Cys Ser Gly Asp Val Thr Tyr His Asp Pro Pro Leu Leu
 595 600 605

Phe Asp Ile Ser Arg Asp Pro Ser Glu Ala Leu Pro Leu Asn Pro Asp
 610 615 620

Asn Glu Pro Leu Phe Asp Ser Val Ile Lys Lys Met Glu Ala Ala Ile
 625 630 635 640

Arg Glu His Arg Arg Thr Leu Thr Pro Val Pro Gln Gln Phe Ser Val
 645 650 655

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Lys Asp Glu Leu

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